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Maximum Match 100%
Listing first 45 summaries
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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
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8: geneseqp2004s:*
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length: 2000000000
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                         2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                            1 MPMYQVKPYHGGGAPLRVEL.....RWMRSCENLAPFNTALKLLK 320
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1667
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(c) 1993 - 2005
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	0	₅	4	ω	2	,_	. NO.	Result
101	101	101	101	101	101	101	102	103	103	103	104	125.5	125.5	125.5	181	214.5	247	832	1191	1378	1630	1630	1667	1667	score	1
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AAU71907	AAB79988	AAB79739	AAU71908	AAB79989	AAB79740	AAR10682	ADS24684	AAM79716	AAM78732	AAU04349	ABB62218	AAG41409	AAG41410	AAG41411	ABG23964	ABB62468	ABP01502	ADR86552	ADR86553	ADC10204	ADR86551	AAW25776	ABM80843	ADE58613	ID	
Aau71907 C. glutam	Aab79988 Corynebac		Aau71908 C. glutam		Aab79740 Corynebac		Ads24684 Bacterial	Aam79716 Human pro	Aam78732 Human pro	Aau04349 Mammalian	Abb62218 Drosophil		0	-		Abb62468 Drosophil	Abp01502 Human ORF	•	Adr86553 84-312 am	Human	Adr86551 1-312 ami	Aaw25776 JTV1 prot	Abm80843 Tumour-as	an P	nescription	

Abm67090	ABM67090	9	104	5.8	96.5	5
Ad191930	3 ADL91930	.5	5215	5.8	97	44
Abb61339	1 ABB61339	21 4	222	5.8	97	ů
Aay77178	AAY77178		559	5.8	97	2
Abp41869	5 ABP41869	52	65	5.8	97.5	1
Ade56502	7 ADE56502		21	5.8	97.5	ô
Aar20033	2 AAR20033		21	5. 8	97.5	39
Ade63088	7 ADE63088		21	5.8	97.5	38
Ade63084	7 ADE63084	.7 7	21	5.8	97.5	37
Add48154	7 ADD48154	7	21	5. 8	97.5	36
Add48158	7 ADD48158	7	21	5.8	97.5	35
Add48150	7 ADD48150		21	5.8	97.5	34
Ade63092	1 ADE63092		217	5.8	97.5	ພ
Aay29621	PAAY29621	2	65	6.0	99.5	32
Aay29614	2 AAY29614		65	6.0	99.5	31
Abu26069	ABU26069		120		100.5	30
Add13589	7 ADD13589		122	6.1	101	29
Aae18908	AAE18908		122	6.1	101	8
Abg80321	5 ABG80321		122		101	27
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ALIGNMENTS

RESULT 1 ADE58613 ADE58613; ADE58613 standard; protein; 320 (first entry) ጅ

29-JAN-2004

Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. Human Protein Q13155, SEQ ID NO 4489.

Homo sapiens.

WO2003016475-A2

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

(GEHO) (FARB) GEN HOSPITAL CORP. BAYER AG.

Woolf C, D'urso D, Befort K, Costigan 3

WPI; 2003-268312/26. GENBANK; Q13155.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal

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cc the expression of a polynucleotide sequence which is differentially compound to the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical compound that regulates the activity of one or more of the cativity in an animal subjected to pain, a method for identifying a compound or small molecule that regulates the activity of one or more of the cativity in an animal of one or more of the polypeptides or identifying a compound useful in treating compound and a pharmaceutical composition comprising the one or more compound useful in treating compound less its activity is useful for preparing the one or more compound in e.g. spinal segmental nerve injury (SNI) in an animal for treating compound (e.g. spinal sequence injury (SNI)) in an animal (e.g. spinal sequence data for the presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: compound that specification, but was obtained in electronic form directly from WIPO at XX
15-APR-2004.
                                                                                                   Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                    WO2004030615-A2
                                                                            Homo sapiens
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Matches
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Conservative 0;
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Pred. No. 5.4e-167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC polypeptides, and their related nucleic acids. The TAT polypeptides and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus coverexpressed in reacer tissues compared to normal tissues, and may thus compared to the tissues of the cancer in compared to the tissues of the cancer in composition and polypeptide and polypeptide compared to the tissues and polypeptide and polypeptide compared to the tissues and tis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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             RWMRSCENLAPFNTALKLLK
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                                                                                          IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ 300
                                                                                                                                                             YQLGFTLIWKNYPKTQMKFSİQTMCPİEĞEĞNİARFLFSİ
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RESULT 2
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RESULT 3 AAW25776

LFGOKHNAVNATLIDSWVDIA

240

180 180 120 120 60 60

300

음 성 밁 Ş 밁 Ś 뭐 Ş В Ś В

100.0%; Pr 100.0%; Pr

Score 1667; DB 8; Pred. No. 5.4e-167;); Mismatches 0;

Indels Length

Gaps

320; 0;

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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JTV1; hPMS2; probe; detection; chromosome 7; deletion;
mismatch repair gene; hereditary non-polyposis colorectal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW25776 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologous recombination.
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                                                                                                                                                                                                                                                                                             MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                               DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                                                                                                                                      DILKRLYELKAAVDGLSKMIQTPDADLDVTNIİQADEPTTLTTNALDLNSVLGKDYGALK 120
                                                                                                                                                                                                                                     DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                            MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 2; 31pp; English
                                                                                                                           YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLEGQKENAVNATLIDSWVDIA 240
RWMRSCENLAPF 312
             RWMRSCENLAPF 312
                                                                              IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ 300
                                                                                                                                                                DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                         YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                                                                                                                                                                                                                                                                                                 97.8%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                Score 1630; DB 2;
Pred. No. 4.3e-163;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting chromosome
                                                                                                                                                                                                                                                                                                                                                           Length 312;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                           240
                                                                                                                                                                180
                                                                                                                                                                                            180
                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                            60
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Ş 문 Ś 문 S

121 121

5 61 Query Match Best Local Sim Matches 312;

Local Similarity

97.8%;

Score 1630; DB 8; ; Pred. No. 4.3e-163; 0; Mismatches 0;

Length 312; Indels

0,

Gaps

Conservative

1 MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD

MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD

DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD

180 120 120 60

DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD

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RESULT 4
ADR86551
ID ADR8
XX ADR8
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                                                          The present invention relates to an isolated p38/JTV-1 protein for use as cc medicament. The p38/JTV-1 protein or the pharmaceutical composition is cuseful as medicament for treating breast cancer, large intestinal cancer, cuseful as medicament for treating breast cancer, large intestinal cancer, cuseful as medicament for treating breast cancer, large intestinal cancer, cc lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cc catalous or intraocular melanoma, uterine sarcoma, ovarian cancer, blood cancer, anal cancer, colon cancer, fallopian tube carcinoma, cendemental carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, cc endogkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue ct tumour, urethral cancer, parathyroid cancer, adrenal cancer, soft tissue clukemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic cancer, bituitary cc cancer, their combination. The protein is useful as a target for corcer, their combination. The present sequence represents the 1-cr amino acid sequence of p38/JTV-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
    Sequence 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-2003; 2003KR-00013058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-312 amino acid sequence of p38/JTV-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR86551 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anticancer agents.
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DB; ADR86548.
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11-JUN-2001; 2001US-0297414F
12-JUN-2001; 2001US-029743F
12-JUN-2001; 2001US-029828F
18-JUN-2001; 2001US-029828F
18-JUN-2001; 2001US-029928F
19-JUN-2001; 2001US-029933F
19-JUN-2001; 2001US-029933F
29-JUN-2001; 2001US-0300883F
28-JUN-2001; 2001US-0300883F
28-JUN-2001; 2001US-0300883F
28-JUN-2001; 2001US-0301530F
28-JUN-2001; 2001US-0301550F
03-JUL-2001; 2001US-0302951F
03-JUL-2001; 2001US-0302951F
28-E2001; 2001US-0302951F
25-EEF-2001; 2001US-0339656F
21-EEB-2002; 2002US-0359656F
21-EEB-2002; 2002US-035903F
22-EEB-2002; 2002US-035903F
22-EEB-2002; 2002US-035903F
22-EEB-2002; 2002US-035964F
01-MAR-2002; 2002US-035964F
01-MAR-2002; 2002US-0363430F
12-MAR-2002; 2002US-0363430F
10-MAR-2002; 2002US-0363430F
10-MAR-2002; 2002US-0363430F
10-MAR-2002; 2002US-0363430F
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06-JUN-2001;
06-JUN-2001;
07-JUN-2001;
07-JUN-2001;
11-JUN-2001;
12-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003000842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predictive medicine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC10204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ 300
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18-NOV-2004

(first entry)

ADR86553 standard;

protein; 229

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84-312 amino acid sequence of p38/JTV-1 protein.
p38/JTV-1; Cytostatic; cancer; leukemia; anticancer

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Best Local S
Matches 268
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 226; 772pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating, preven associated disor or CNS diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK,
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
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                           LOQIGGCSVTVPANVQRWMRSCENLAPF 312
                                                                                    HNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSV
                                                                                                                                                      LLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQK 224
                                                                                                                                                                                                    ALDINSVLGXDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURAGEN CORP.
                                                            HNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSV
                                                                                                                                  LLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQK
                                                                                                                                                                                                                          ALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPEN
                                                                                                                                                                                                                                                                                              QEESNLSLQALESRQDDILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTN
                                                                                                                                                                                                                                                                                                                                                                                                                   272 AA;
                                                                                                                                                                                                                                                                        QEESNLSLQALESRODDILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTN
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lepley DM;
                                                                                                                                                                                                                                                                                                                                                              82.7%;
                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                            Score 1378; DB 7;
Pred. No. 1.6e-136;
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                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                 272;
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                                                                                                                                  184
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RESULT 7
ADR86552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to an isolated p38/JTV-1 protein for use as CC medicament. The p38/JTV-1 protein or the pharmaceutical composition is CC useful as medicament for treating breast cancer, large intestinal cancer, CC lung cancer, small cell lung cancer, scomach cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, CC cutaneous or intraocular melanoma, uterine searcoma, ovarian cancer, CC endometrial cancer, colon cancer, fallopian tube carcinoma, CC endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, CC endometrial cancer, parathyroid cancer, small intestine cancer, soft tissue CC tumour, urethral cancer, parathyroid cancer, prostate cancer, chronic or acute CC cutanemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter CC cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary CC adenoma, or their combination. The protein is useful as a target for CC screening new anticancer agents. The present sequence represents the 84-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
              18-NOV-2004
                                               ADR86552;
                                                                               ADR86552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 6; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADR86550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anticancer agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-2003; 2003KR-00013058.
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                                                                                                                                                                      181
                                                                                                                                                                                                      264
                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                         204
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                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                          DADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                    GKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQRWMRSCENLAPF
                                                                                                                                                                                        GKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQRWMRSCENLAPF 312
                                                                                                                                                                                                                                       MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                             MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMSAL
                                                                                                                                                                                                                                                                                                          EHFRYLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQT
                                                                                                                                                                                                                                                                                                                                 EHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQT
                                                                                                                                                                                                                                                                                                                                                                               DADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                             protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%; Score 1191; DB 8; 100.0%; Pred. No. 7.2e-117;
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RESULT 8
ABP01502
ID ABP0
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AC ABP0
XX
AC ABP0
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AC ABP0
XX
XX
AX

ABP01502 standard;

protein;

51

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120 120

60 60

24-JUN-2002 ABP01502;

(first entry)

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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 5; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAR-2003; 2003KR-00013058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-161 amino acid sequence of p38/JTV-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1454628-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYSE-) UNIV SEOUL NAT IND FOUND
                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%;
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121
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                                                                                                                                                                                                                                                                                                                        161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                        DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                              DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV 161
                                                                                                                                                                                                           MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                                                                                                                MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
  DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV
                                                                                                 DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                          49.9%;
                                                                                                                                                                                                                                                                                                                     Score 832; DB 8; ; Pred. No. 3.9e-79; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Length 161;
                                                                                                                                                                                                                                                                                                                        Indels
  161
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(first entry)

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RESULT 9
ABB62468
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                                                                                                                                                                        CC (referred to as open reading frame, ORPX, where X is 1-1149] (see Table 1 CC (referred to as open reading frame, ORPX, where X is 1-1149] (see Table 1 CC in the specification). ABN15762 to ABN27252 encode the human ORPX CC proteins given in ABP00010 to ABN27252 encode the human ORPX CC treating or preventing a pathology associated with an ORPX-associated of the pathology associated with an ORPX-associated syndrome associated with ORPX-associated disorder. ORPX polynucleotide compared to the concert of cancer, hyperproliferative disorders. ORPX polynucleotide constending tumours, keloid, degenerative disorders, haemorrhage, considered respective disorders, haemorrhage, constead thation, cardiovascular diseases, diabetes mellitus, systemic considerations, hypertension, hypertension, hyperthyroidism, cholesterol ester consteads, autoimmune disorders such as multiple sclerosis, infectious for storage disease, various immune deficiencies and disorders, infectious storage and autoimmune thyroiditis, myastchenia gravis, graft-versus-host consequence and autoimmune thyroiditis, myastchenia gravis, graft-versus-host consequence disorders, incisions, ulcers, for treating osteoporosis, consecutive disorders, and for gut reperfusion injury in various tissues and conditions resulting from the printed specification, but was obtained in electronic compared to the printed specification, but was obtained in electronic compared to the printed specification, but was obtained in electronic compared to the printed specification.
                                                                                                                   Query Match
Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 2986; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX protein sequence
                                                                                    74
                                                           Н
                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-106308/14.
DB; ABN17254.
                                                                                                                              Similarity
                                                    DGLSKMIQTÞDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVI 124
                                      bólskvíthtébáblbýtivíldábeettílttválblnsvíkkotkalkotví 51
                                                                                                             Conservative
                                                                                                                      14.8%;
96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; autoimmune
                                                                                                    Score 247; DB 5;
Pred. No. 4.5e-18;
1; Mismatches 1
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                                                                                                                             Length 51;
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                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                               Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 14196; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
N-PSDB; ABL06571.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 14196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
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                                                                                   160
                                                                                                                124
                                                                                                                                             100
                                                                                                                                                                        73
                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                   Similarity
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acid detection reagent for detecting 1000 or more and for elucidating cell signaling and cell-cell

English.

invention is

E. PWD,

Myers Œ₩,

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270 AGNELTVADVVLWSVLQQIGGCSVTVPANVQR 301
                                                                                                                                                                                                                                                                                         13 IKLPTCWYPLKNVSLAADSLASGSSTSASTSSCKLEANRIDRTGRNAATCALDLDS
                       I IRYLGRVGPAEYRYEGSPLCNEIDLVLDICYQLLRCNTHKTQVAMVRLLDKRLQKQQYF
                                                      IARFLFSLFGOKHNAVNATL---IDSWVDIAIFOLKBGSSKBKAAVFRSMNSALGKSPWL
                                                                                        DIGPAAREFEANLAKV--PVNPALPK----ISVTLIWKYCEHTEMISSPTMYVPIYGEVN
                                                                                                                      SV------PENILIKCFGEONKKOPRODYQLGFTLIWQVDKTONKFSIQTMCPIEGEGN
                                                                                                                                                                                   TLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHPRVLSTVHTHSSVK 159
                                                                                                                                                                                                                        LGRQIQRLLKDDTASVAARQEKVLKQLEELKAQLGQIR-----AGLGVCG--KTFQHT
                                                                                                                                                                              TAFQNG----
                                                                                                                                                                                                                                                        VELPTCMYRLPNY----HGRSYGPAPGAGHVQEESNLSLQA-----
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                12.9%; Score 214.5; DB 4;
25.6%; Pred. No. 2.8e-13;
tive 50; Mismatches 120;
                                                                                                                                                        -GLKEVPLQDVVÍNGHÉNFI ÞYALLALKNAWRNLYTIDVKTFTHSTWA
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                                                                                                                                                                                                                                                                                                                                                                                             Length 334;
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Minimum
Maximum
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                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                           DB DB
                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Patent No. 5194600	sequence 18, Appr	9 0	è.	σ.	e 6834	Sequence 13, Appl	13,	4	Α,	'n	2,	e 62,	11178	Sequence 736, App	e 10	Sequence 2, Appli	e 203	e 1,	e 1,	e 1,	e 1,	,2	Sequence 4, Appli	e 10,	48	Sequence 2, Appli	nce 113	Description	

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82.5	83	83	83	83	83	83.5	83.5	84.5	84.5	84.5	84.5	84.5	84.5	85	85	85.5	86
4.9	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.2
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US-09-248-796A-18146	US-09-606-304-8	US-08-836-567-8	US-09-989-786-1	US-09-385-742B-1	US-09-052-339-1	US-09-107-433-3893	US-09-583-110-3930	US-08-446-550-2	US-08-446-549-2	US-08-445-186-2	US-08-220-674-2	US-07-670-611-2	US-09-107-433-4488	US-08-469-537A-97	US-10-253-509-1	US-09-357-251-37	5194600-4
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No. 5194600
18146, A	8, Appli	8, Appli	1, Appli	1, Appli	1, Appli	3893, Ap	3930, Ap	Appli	2, Appli	2, Appli	2, Appli	2, Appli	4488, Ap	97, Appl	1, Appli	37, Appl	5194600

ALIGNMENTS

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US-09-949-016-11312
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Best Local S
Matches 320
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 11312
LENGTH: 3411
TYPE: PRT
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 1667; DB 4; Length 341; Local Similarity 100.0%; Pred. No. 2.4e-181; les 320; Conservative 0; Mismatches 0; Indels 0
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RWMRSCENLAPFNTALKLLK 320
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                                                                        IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ 321
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RWMRSCENLAPFNTALKLLK 341

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; MOLECULE TYPE: protein
US-08-518-862C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acids
TYPE: linear
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Best Local Similarity 100.
Matches 312; Conservative
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US-08-518-862C-2
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Patent No. 5943757
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Hicolaides, Nicholas C.
TITLE OF INVENTION: Human JTV1 Gene Overlaps PMS2 Gene
JUNBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: river, COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
The compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the
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FILING DATE: 24-AUG-1995
CLASSIFICATION: 435
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STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
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RWMRSCENLAPF 312
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                                                                                                       IFOLKEGSSKEKAAVERSMNSALGKSEWLAGNELTVADVVLWSVLQQIGGCSVTVEANVQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.8%; Score 1630; DB 2; Length 312; 100.0%; Pred. No. 3.5e-177; ative 0; Mismatches 0; Indels
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APPLICANT: Countingham, Mary Jane
APPLICANT: Zweiger, Gary
APPLICANT: Zweiger, Matthew R.
APPLICANT: Benzer, Scott
APPLICANT: Seilhammer, Jeffrey J.
APPLICANT: Baughn, Mariah
APPLICANT: Baughn, Mariah
APPLICANT: Azimzai, Yalda
APPLICANT: Lal, Preeti
ITITLE OF INVENTION: WAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
CURRENT APPLICATION NUMBER: US/09/443,184A
CURRENT FILING DATE: 1999-11-19
SOFTWARE: PERL PROGram
SEQ ID NO 48
LENGTH: 1512
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-756-317-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
                                                                                                                                      APPLICANT: Clemente, Thomas E.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Mitsky, Timothy A.
APPLICANT: Stark, David M.
TITLE OF INVENTION: Improved Rhodospirillum Rub
TITLE OF INVENTION: Poly-B-Hydroxyalkonoate Syr
NUMBER OF SEQUENCES 15
CORRESPONDENCE ADDRESS:
ARTOId, White & Durkee
STREET: P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                             Sequence 10, Applications Patent No. 5849894
GENERAL INFORMATION:
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US-09-443-184-48
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48,
Patent No. 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1
                                                                                                                    STREET: P.O. B
CITY: Houston
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 6.2%;
Local Similarity 22.1%;
les 45; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 KQKKAPVHVKRWFGFLEAQQAPQS 162
                                                                                                                                                                                                                                                                                                                                                                        10, Application US/08756317
o. 5849894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 INANPASPPLSLĻVLHRĻLCEHERVLSTVHTHSSVKSVPENLĻKCFGEQNKKQPRQDYQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 DIAIFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 GFTLIWKNVPKTOMKFSIQTMCPIEGEGNIARFL-----FSLFGOKHNAVNATLIDSWV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 EFSATKL--SSCDSFTSTINELNHCLSLRTYLVGNSLSLADLCVWATLK--GNAAWQEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 ----VSENVIFTDV------NSILRYLARVATTAGLYGS--NLMEHTEIDHWL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --VTVPANVQRWMRSCENLAPFNT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8, Application US/09443184A
6372431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 103; DB :
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Indels
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292

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Mol
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 2000000000
Published Applications AA:*

1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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4: /cgn2=6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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18: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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19: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

20: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-622-817-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (without alignments)
2084.158 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1380268
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	12 100.5	11 100.	10 10	9 10	8 101	7 1(6 10	5 10	4 10	3 83	2 119	1 163	Result No. Score
					01 6.1					32 49.9		30 97.8	:
,	1200	687	1221	1221	1221	1221	833	826	201	161	229	312	Query Match Length DB
'n	15	15	17	15	9	9	10	10	15	16	16	16	8
	US-10-282-122A-53993	US-10-425-114-58897	US-10-494-675-156	US-10-450-055-2	US-09-738-626-5163	US-09-919-891-2	US-09-746-660A-90	US-09-746-660A-92	US-10-369-493-13717	US-10-463-676-5	US-10-463-676-6	US-10-463-676-4	ID
Semience 2001 25	Sequence 53993, A	Sequence 58897, A	Sequence 156, App	Sequence 2, Appli	Sequence 5163, Ap	Sequence 2, Appli	Sequence 90, Appl	Sequence 92, Appl	Sequence 13717, A	Sequence 5, Appli	Sequence 6, Appli	Sequence 4, Appli	Description

45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
	_	92	92	93.5	93.5	94	94	94	94.5	95	95	95	95	95	95	95	95	95	95.5	96	96.5	g	97	97	97	97	97	97	97	97	97.5
5 5								5.6					5.7	•			5.7			•	5. 8	•	•		•	•	•	•	•		
1192	1149	1206	739	733	569	1440	468	203	955	936	722	559	559	559	559	559	559	559	455	606	1148	914	5215	5215	5215	5215	5215	856	856	559	711
15	6	15	15	15	16	16	15	15	15	14	15	17	14	14	14	14	9	9	15	16	16	16	14	10	10	9	9	9	9	9	16
-10-282-122A-	-10-655-799-30	-10-282-122A-6383	-10-424-599-25152	-10-424-5	-10-437-963	-10-437-963	0-424-599-	-10-369-49	82-122A	85-7	-10-369-4	-10-91	-10-252-518-	-10-266-787-	US-10-259-632-1		820-	US-09-821-016-1	-10-425-114-4263	Ψ	-10-655-799-	-10-437-963-1	-10-271-88	-09-836-821-	US-09-988-384B-2	-09-860-846-	-09-861-28	-09-364-847-3	-09-364-847-	64-847-2	US-10-437-963-175483
e 64644,	e 30, A	ው	e 25152	ø	e 12390	Sequence 136277,	e 260388	Φ	æ	e 7442,	10	,-	Ļ	,-	Sequence 1, Appli	e 1,	1,	1, Appl	æ	æ	æ	e 153	e 45,	e 2, Appl	ce 2,	equence 2,	e N	e y	equence 33	2	Sequence 175483,

ALIGNMENTS

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FILE REFERENCE: 012679-091
CURRENT APPLICATION NUMBER: US(10/463,676.)
CURRENT FILING DATE: 2003-06-76
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
NUMBER OF SHO ID NOS: 17
SOFTWARE: FabtSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 312
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                                                                                                                                                                                                                                                               ; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(312)
; OTHER INFORWATION: 1-312 amino acid sequence of p38/JTV-1
US-10-463-676-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-10-463-676-4
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Publication No. US20040175375A1
GENERAL INFORMATION:
                                                                                                                                                                        Matches
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kim, Sunghoon
APPLICANT: Park, Bum-Joon
TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating Cancer
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                   / Match 97.8%; Score 1630; DB 16; Length 312;
Local Similarity 100.0%; Pred. No. 6.4e-153;
nes 312; Conservative 0; Mismatches 0; Indels 0
                           61
                                                                                                        1 MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
DILKRLYELKAAVDGLSKMIQTPDADLDVINIIQADEPTTLTINALDLNSVLGKDYGALK 120
                                                                            MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
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RESULT 3
US-10-463-676-5
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US-10-463-676-6
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Sequence 5, Application US/10463676
Publication No. US20040175375A1
GENERAL INFORMATION:
APPLICANT: Kim, Sunghoon
APPLICANT: Park, Bum-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Park, Bum-Joon
TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating Cancer
FILE REFERENCE: 012679-091
CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 229
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10463676 Publication No. US20040175375A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Matches 229;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE
LOCATION: (1)...(229)
OTHER INFORMATION: 84-312 amino acid sequence p38/JTV-1
                                                                                                                                                                    264
                                                                                                                                                                                                    121
                                                                                                                                                                                                                              204
                                                                                                                                                                                                                                                                            144 EHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKVVPKTQMKFSIQT
                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                       84 DADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPELSLLVLHRLLC
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                                                                                                                                                                 GKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQRWMRSCENLAPF 312
                                                                                                                                                                                                                MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMVSAL
                                                                                                                                    DIVINANPAS PFLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                                                                                                                                                                        EHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQT
                                                                                                                                                                                                                                                                                                                       DADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWMRSCENLAPF 312
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                              71.4%;
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                              Score 1191; DB 16;
Pred. No. 1.5e-109;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                    Matches
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                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo |
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 161
                                                                                                                                                                  Local
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; TYPE: PRT ; ORGANISM: Pseudomonas fluorescens US-10-369-493-13717
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13717
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating FILE REFERENCE: 012679-091
CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR PRILING DATE: 2003-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
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OTHER INFORMATION: 1-161 amino acid sequence of p38/JTV-1
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                                                                                              GPAAARLITVÉGAKFNAEEVITRAHNFLKV----
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5; Mismatches
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86	86.5	86.5	86.5	86.5	86.5	87	87.5	87.5	87.5	87.5	87.5	88	88	88	88.5
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hypothetical prote	MAD1 protein - yea	unknown protein (i	translation elonga	methyl-accepting c	glutathione transf	ctp synthase (pyrG	hypothetical prote	multifunctional am	probable magnesium	SEC8 protein - yea	glutathione transf	translation elonga	glutathione transf	conserved hypothet	rho-type GTPase-ac

ALIGNMENTS

probable glutamate-tRNA ligase (EC 6.1.1.17) F21E10.12 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Becies: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T01200 R;Davidson, S:; Rohlfing, T:; David, M.; O'Brian, D. submitted to the EMBL Data Library, April 1998 A;Description: The sequence of A. thaliana F21E10. A;Reference number: Z14258 A;Accession: T01200 A;Retatus: translated from GB/EMBL/DDBJ A;Molecula type: DNA A;Residues: 1-728 <DNA A;Residues: 1-728 <DNA A;Residues: UNIPROT:065253; EMBL:AF058914; NID:g3047074; PID:g3047084; GSPDB:GNC C;Genetics: probable glutamate-tRNA ligase (EC 6.1.1.17) [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress) C.Jate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004 C.Accession: TS2043 R.Day, T.S.; Golovkin, M.; Reddy, A.S. Biochim. Biophys. Acta 1399, 219-24, 1998 A.Fitle: Cloning of the CDNA for glutamyl-tRNA synthetase from Arabidopsis thal A.FReference number: Z24836; MUID:9765600; PMID:9765600 A.Accession: TS2043 A.Scession: TS2043 A.Status: preliminary; translated from GB/EMBL/DDBJ A.FRefuse: 1-719 cDAY A.FRESIOUS: preferences: UNIPROT:082462; EMBL:AF067773; PIDN:AAC36469.1 C.Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology C.FKeywords: ligase S S 밁 밁 Matches Query Match N Local 247 GSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLMSVLQQIGGCSVTVPANVQRW 302 188 IWKNVPKTQMKFSIQIMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA-IFQLKE 128 PASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTL 187 94 56 LLRYV------GRSAKKLPDFYG--NNAFDSSQIDEWVDYASVF--SS 10 48; Similarity GSEFENAC--GRVDKYLESSTFLVGHSLSIADVAIWSALAGTG------PESPPLSVIVALSLSASPV----TIDSSAAATTVPSFV---FSDGRKLN-----GATV Conservative 7.5%; 26; Score 125.5; DB Pred. No. 0.017; Mismatches DB 2; 53; Indels Length 719; Arabidopsis thaliana 49; Gaps 137 246 ភូ 93 9

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RESULT 4
A29036
glutathione transferase (EC 2.5.1.18) yb3 -
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-De
C;Accession: A29036
C;Accession: 4.716-1-15
     R Abramovitz, M.; Listowsky, I.
J. Biol. Chem. 262, 7770-7773,
A;Title: Selective expression o
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A; Map position:
C; Superfamily: 1
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G82441
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A;Molecule type: DNA
A;Residues: 1-222 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable glutathione S-transferase VCA0584 [imported] - Vibrio cholerae (st. C;Species: Vibrio cholerae (st. C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: G82441.
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A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis P;223-499/Domain: glutamine-tRNA ligase homology <EGL>
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;Superfamily: hypothetical protein b2302
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                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                        EVMDGQLAQNPYLAGDEYTIADIATFPWVRIHEWSGISIDGLTHLQRWM
                                                                                                                                                                                                                        RSMNSALGKSPWLAGNELTVADVVL--WSVLQQIGGCSVTVPANVQRWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                          LMFQMSGVGPMMGQANV---FYRYFPEKIQPA----IDRY------QKEGRRLF
                                                                                                                                                                                                                                                                                           MKFSIQIMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QRW 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YASVF--SGSEFENAC--GRVDKYLESSTFLVGHSLSIADVAIWSALAGTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IA-IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLRYV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNAT-----LIDSWVD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PESPPLSVIVALSLSASPV----TIDSSAAATTVPSFV---FSDGRKLN-----GATV 55
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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25.9%;
     , 1987
of a unique
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Pred. No. 0.17;
2; Mismatches
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                                                                         28-Dec-1987
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     S-transferase
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H.; Dragoi,
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     Yb3
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I.; Sellers,
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A; Molecule type: mRNA
A; Residues: 1-645 <VAL>
A; Residues: 1-645 <VAL>
A; Residues: 1-645 <VAL>
A; Cross-references: GB: U78524; NID: g1696006; PIDN: AAB58488.1; PID: g1696007
A; Note: it is uncertain whether Met-4 or Met-6 is the initiator
C; Comment: This protein is localized to the nucleus and interacts with Gu/RNA helicase
C; Koywords: phosphoprotein
F; 50-58/Region: nuclear location signal
F; 362-374/Region: nuclear location signal
F; 362-374/Region: nuclear location signal
F; 514-517,551-554,592-595,606-609/Region: 4-residue repeats (N-T-S-L)
F; 7,177,322,412,432,460,461,462,470,614,627/Binding site: phosphate (Ser) (covalent) #s
F; 65,394,624/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Valdez, B.C.; Henning, D.; Perlaky, L.; Busch, R.K.; Bus Blochem. Blophys. Res. Commun. 234, 335-340, 1997
A;Title: Cloning and characterization of Gu/RH-II binding A;Reference number: JC5517; MUID:97320420; PMID:9177271
A;Accession: JC5517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A29036; MUID:87222405; PMID:3584141
A;Accession: A29036
A;Accession: A29036
A;Molecule type: mRNA
A;Residues: 1-218 (ABR)
A;Cross-references: UNIPROT:P08009; GB:J02744; NID:g204512; PIDN:AAA41292.1;
C;Superfamily: glutathione transferase
C;Keywords: transferase
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 -----LIDSWVDIA-----IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 QDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 EKFKLG--LDFPNLP-----YLIDGSHKITQSNAILRYL----GRKHNLCGETEEERIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
      AIFQLKEGSS
                                                                                                                                                                                                                                                                                                                                   DGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPPL
                                                                                                                                                                                                           LPVSLLGPKHELELPHLTSALHPVHPDIKLQKLPFYDLLDELIKPTSLASDNSQRFRETC
                                          KPCSLPGYLPPTKNGVEPKRPSRPINITSLV----
                                                                                                                          FAFALTPQQVQQISSSM----DISGTKCDFTVQVQLRFCLSETSCPQEDHFPPNLCVKVNT
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                                                                                                                                                                     ----PRQDYQLGFTLIWKNVPKTQMKFSIQ-----TMCPIEGEG------
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                                                                                                                                                                                                                                                 -SLL-VLHRLLCEHF-RVLSTVHTHSSVKSVP----ENLLK--CFGEQNKKQ-----
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                                                                                                                                                                                                                                                                                                  ADLSIPNVHSSPMPATLSPS----
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KEKAAVFRSMNSALGKSPWLAGNELTVADVVL-WSVLQQIGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 97.5;
Pred. No. 3.
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                                                                              ---NIARFLFSLFGQKHNAVNATLIDSWV-----DI
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                                          -RLSTTVPNTIVVSWTAEIGRNYSM
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Q9KUM6
Q8KW4
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Q8ETT1
Q8ETT1
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SYEP MOUSE
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	ALIGNMENTS	GTM3_RAT	Q66CB1	Q8EGM4	Q6W112	PIA1_MOUSE	Q6NH83	Q6UDR4	Q8NQD1	Q6M580	Q6TXE9	Q88D25	Q8KQ23	Q9LIZ8	Q87XN7	
		P08009 rattus norv	Q66cbl yersinia ps	Q8egm4 shewanella	Q6w112 rhizobium s	O88907 mus musculu	Q6nh83 corynebacte	Q6udr4 mus musculu	Q8nqd1 corynebacte	Q6m580 corynebacte	Q6txe9 rattus norv	Q88d25 pseudomonas	Q8kq23 pseudomonas	Q9liz8 oryza sativ	Q87xn7 pseudomonas	

A TO POPO CON REPRESENTATION OF A PART OF A CONTROL OF A PART OF A CONTROL OF A PART OF A CONTROL OF A PART OF A PAR RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Klausher R.D., Collins F.S., Wagner L.H., Derge J.G., RA Klausher R.D., Collins F.S., Wagner L.A., Schaefer C.F., Bhat N.K., RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Bonaldo M.F., Casaavant T.L., Scheetz T.E., RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. [4] MEDLINE=96115582; PubMed=8666379; Nicolaides N.C., Kinzler K.W., Vogelstein B.; "Analysis of the 5. region of PMS2 reveals heterogeneous transcripts and a novel overlapping gene."; Genomics 29:329-334(1995). Name-JTV1; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCA2 HUMAN STANDARD; PRT; 320 AA. Q13155; Q9P1L2; Q1-201 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Multisynthetase complex auxiliary component p. (PRO0992). Zhang C., Yu Y., Zhang Liu M., He F.; SEQUENCE FROM N.A. TISSUE=Lymph; NCBI_TaxID=9606; TISSUE=Fetal SEQUENCE FROM N.A. SEQUENCE OF 197-320 liver; FROM N : : Wei Craniata; Vertebrata; Euteleostomi; Ξ. Zhou . G Ouyang p38 (JTV-1 protein) ; S Luo ۲. 멆 human

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RESULT 2
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Q96CZ5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U24169; AAC50391.1; ALT_FRAME.
EMBL; BC002853; AAH02853.1; -
EMBL; BC010156; AAH10156.1; -
EMBL; AF116615; AAF71039.1; -
H-InvdB; HIX0006460; -.
MIM; 600859; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure. Mediates ubiquitihation of FUBP1 and its degradation )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJNE=22716800; PubMed=12819782; DOI=10.1038/ng1182; Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W., Lee S.W., Han J.W., Lee H.-W., Kim S., "Downregulation of FUSE-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation."; Nat. Genet. 34:330-336(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH FUBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the processome.

SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43. Binds FUBP1.

SIMILARITY: Contains 1 GST-like domain.
CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 312.
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                                                                                                                                                                                YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSIFGQKHNAVNATLIDSWVDIA
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Pred. No. 6e-127;
Mismatches 0;
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                                                                                                                                                                  EGEGNIARFLFSLFGOKHNAVNATLIDSWVDIA
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.T. Marra M.A.,
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013630; AAH13630.1;
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
InterPro; IPR010987; GST_C_like.
SEQUENCE 320 AA; 35335 MW; 19F14BF758612E08 CRC64;
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Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Theria; Primates; (
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Pred. No. 1.
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Last sequence update)
Last annotation updat
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RC STRAIN=TVB/N, and FVB/N-3; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Histeh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

RA Rodriguez A.C., Stabska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local S
Matches 279
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Q8R010;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2002) to the EMEBL; BC024410; AAH24410.1; -. EMBL; BC026972; AAH26972.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-FVB/N-3; TISSUE-Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:2385237; Jtv1.
InterPro; IPR004046; GST_Clike.
InterPro; IPR010987; GST_C; 1.
F£am; PF00043; GST C; 1.
SEQUENCE 320 AA; 35396 MW; 1
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YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQYHNAVNATLIDSWYDIA
                                                                                                                    DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                                                                                                                                                                        DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                                                                           MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                                                                                                                                                                                DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
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Rodentia;
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87.2%;
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Pred. No. 1.
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XX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Altschul S.F., Jordan H., Moore T., Ax S.I., Wang J., Hsieh F.,

XX Altschul S.F., Jordan H., Moore T., Ax S.I., Wang J., Hong L.,

XX Altschul S.F., Waller M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Altschul S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Altschul S.F., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

XX Altschul S.F., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

XX Altschul S.F., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

XX Altschul S.F., Worley K.C., Hale S., Garcia A.M., Schein S., Sanchez A.,

XX Altschul S.F., Worley K.C., Hale S., Garcia M.A., Rodrigues S., Sanchez A.,

XX Altschul S.F., Worley A.C., Shevchenko Y., Boutfard G.G.,

XX Altschul S.F., Worley A.C., Shevchenko Y., Boutfard G.G.,

XX Altschul S.F., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

XX Altschul S.F., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Q8R2Y6;
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01-MAR-2004
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Name=Jtul;
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
SEQUENCE 320 AA; 35423 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CZECH II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #GI:2385237; Jtv1.
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121
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                                                                                             DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                         DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
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                                                                                                                                                                                   MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTNPATDAGHVQETSEPSLQALESRQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences."
l. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                       87.8%;
87.2%;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                       Score 1464; DB 2;
Pred. No. 1.8e-110;
6; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1C21F1A74C9882B4 CRC64;
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InterPro; IPR010987; GST C 11ke.
InterPro; IPR004046; GST_Cterm.
Pfam; PF00043; GST_C; 1.
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identification of protein-protein interactions a core protein.";
J. Mol. Biol. 285:183-195(1999)
-I-FUNCTION: Probable core protein of the mult that serves as a template for the assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=9906915; PubMed=9878398; DOI=10.1006/jmbi.1998.2316; Quevillon S., Robinson J.-C., Berthonneau E., Siatecka M., Mirande "Macromolecular assemblage of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Multisynthetase complex auxiliarry component p38.
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10029;
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                                                                                                                                                                                                                                                                                                                                                                               Structure.
SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyf-rRNA synthetase, the monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43.
SIMILARITY: Contains 1 GST-like domain.
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                                                                                                                               Similarity
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E 320 AA; 3
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 DILKRLYELKAAVDGLSKMIQTEDADLDVTNIIQADEFTTLTTNALDLNSVIGKDYGALK
                                                              MEMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESROD
                                             MPMYÖVKSYHGGSAÞLRVELÞTCMYRLÞNVHSKTTSÞATDÁGHVÖETSEÞSLQALESRÓD
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                                                                                                                 Conservative
                                                                                                                                                                            ΑA;
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                                                                                                                            86.6%;
                                                                                                                                                                         35433 MW;
                                                                                                               16;
                                                                                                          Score 1444; DB 1;
Pred. No. 7.6e-109;
6; Mismatches 27;
                                                                                                                                                                     6D24E033ABEC810A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the multisynthetase complex
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                 Query Match
Best Local Sim
Matches 243;
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RC STRAIN=FVBNN; TISSUE=Mammary tumor. C3;

RX MEDLINE=22388257; PubMed=12477932; DDI-0.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McCEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2002) to the
EMBL; BC024480; AAH24480.1;
MGD; MGI:2385237; JTV1.
                                                                                                                                                                                                                                                                                                                                                                                              With Marra M.A., Jones S.J., Marra M.A., Generation and initial analysis of and mouse cDNA sequences."; and mouse cDNA sequences.";
                                                                                                                                                            Pfam;
                                                                                                                    InterPro; IPRO04046; GST_Cterm.
InterPro; IPRO10987; GST_C like.
Pfam; PF00043; GST_C; 1. -
Pfam; PF00043; GST_C; 1. -
Pfam; PF00043; GST_C; 1. -
                                                                                                                                                                                                                                                                                                                                          STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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01-JUN-2002
01-JUN-2002
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Mammalia; Eutheria; Rodentia;
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Mus musculus (Mouse).
Musculus (Mouse).
Chordata;
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                                                                                                                                                                                                                                                                                                                               FROM N.A.
VB/N; TISSUE=Mammary tumor.
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                 Conservative
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                                                                                                            31097 MW; E5BE81498983FD2E
                                     75.6%; Score 1260; 88.0%; Pred. No. 5.
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Last sequence update)
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Sciurognathi; Muridae; Murinae; Mus
           Mismatches
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                                  5.5e-94;
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                                                      Length 280;
        Indels
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RX Alischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Alischul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Kong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Kong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Kong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Kong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Kong L.,
RX Diatchenko L., Marusina M.F., Casaninci P., Prange C.,
RX Diatchenko L., Wadin T.B., Toshiyuki S., Carminci P., Prange C.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,
RX Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RX Richards S., Worley K.C., Schibbs R.A.,
RX Richards S., Worley K.C., Schibbs R.A.,
RX Richards S., Wor
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Matches 220
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ
EMBL; BC074561, AH74561.1;
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010997; GST_C_11ke.
Pfam; PP00043; GST_C; 1.
Pfam; PP00043; GST_C; 1.
Pfam; PP00643; GST_C; 1.
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xen
NCBI_TaxID=8364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
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                                        Conservative
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                                                                        68.7%;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Hohey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hohey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Karywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
RA Arnes S.J. Marra M.A.
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Jones S.J., Marra M.A.;
"Generation and initial analysis of and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:168
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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RX MEDITALE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
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Best Local Sim!
Matches 221;
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Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                     Q7ZYD7;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                 TISSUE=Embryo;
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                               Q7ZYD7
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ da
EMBL; BC072178; AAH72178.1; -.
InterPro, IPR004046; GST Cterm.
InterPro, IPR010987; GST Clike.
Pfam; PF00043; GST C; 1. - -
Pfam; PF00043; GST C; 1. - -
SEQUENCE 311 AA; 34424 MW; D5E8325C18D88751
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TISSUE=Ovary;
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Matches 221
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC043832; AAH43832.1; -
InterPro; IPR000446; GST Cterm.
InterPro; IPR010987; GST Clike.
Pfam; PF00043; GST C; 1.
SEQUENCE 311 AA; 34647 MW; 2F08C9DA60DD63BE CRC64;
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TISSUE=Embryo;
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MEDLINE=22341132;
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9; Mismatches 51;
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r L., Pontius J., Clifton S.W.,
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SEQUENCE FROM N.A.

TISSUE-Kidney;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler (
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.)

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Q7T3C0 Q7T3C0; Q7T3C0; 01-OCT-2003 01-OCT-2003 01-MAR-2004

(TrEMBLrel. 25, 13 (TrEMBLrel. 25, 14 (TrEMBLrel. 26,

Created)
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Zgc:63976. ORFNames=zgc:63976;

Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID=7955;

) (Danio rerio). ; Craniata; Vertebrata; Eu Teleostei; Ostariophysi;

Euteleostomi;

Cypriniformes;

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AD Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

AN Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

AN Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AN Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

AN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

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AN Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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AN Hiting M., Madan J.W., Green E.D., Dickson M.C.,

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AN Hiting M. Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences ";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Best Local Similarity
Matches 184; Conserv
                                                                                                                                                                  O707A3 PRELIMINARY;
Q707A3;
01-MAR-2004 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ database:
EMBL; BC053178; AAH53178.1; -.
ZFIN; ZDB-GENE-040426-2652; zgc:63976.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR004987; GST_Clike.
Pfam; PF00043; GST_C; 1.
Pfam; PF00043; GST_C; 1.
SEQUENCE 321 AA; 34852 MW; BA8F6B951208244A CRC64;
                                                  Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                      AGCP5808 (Fragment).
Name=agCG50514; ORFNames=ENSANGG00000011827;
  SEQUENCE
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TISSUE-Kidney;
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WEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gaclayne J.D., A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ashril J.F., Agbayani A., Baxeer E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Bellew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Abardis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra R., Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W., Fosler C., Gabriellan A.E., Garg N.S., Gebbart W.M., Glasser K., An Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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EMBL, AAAB01008960; EAA10870.1; -.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an
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pred. No. 2.6e-
47; Mismatches
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Query Match
Best Local S
Matches 85
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RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Lialai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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                                                                               EMBL; AE003530; AAS64998.1; -.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR001997; GST_C_like.
Pfam; PF00043; GST_C; 1.
SEQUENCE 301 AA; 33241 MW; 3
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SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                    Biol.
                                 Similarity
                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                FROM
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                                                                                                                                                                                                                                                          (SEP-2002)
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             47;
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     Score 224; DB 2;
Pred. No. 7.6e-10;
7; Mismatches 120;
                                                                             35224E17FE03F3BE CRC64;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson of Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., F., Mirande M., Gonzalez M., Guarin H., Kronmiller B., Li P., Li Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rub.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
NON TRR
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Meoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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LP12114p (Fragment).
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot
Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                   AIFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV----PENLLKCFGEQNKKQPRQDYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAQLGQIR-----AGLGVCG--KTFQHTTAFQNG-----GLKEVPLQDVVINGHPN
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F
                                                  STANDARD;
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Last sequence update)
Last annotation updat
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Pred. No. 8.
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                                                  334
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.3e-10;
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     RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Godayne J.D.,
RA Adams M.D., Celniker S.E., Hilt R.A., Evans C.A., Godayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q. Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q. Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Colson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Gann P., Harris M.,
RA Harris N.L., Harvey D.A., Heinan T.J., Hernandez J.R., Houck J.,
Harvis C., Gabrielian A.E., Garg N.S., Gelbart M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M., Glasser K.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
RA Merkulbov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulbov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulbov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Shue B.C., Stden-Kiames I., Simpson M., Skupski M.P., Saith T.,
RA Shue B.C., Stander S., Zhan M., Shung S., Yao Q.A.,
RA Wang X.-, Wei R.-, Zaveri J.S., Zhan M., Zhang G. Zhao Q. Zheng L.,
RA Yel R.-, P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Ra Yel R.-, P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Ra Yel R.-, P., Ra Yell R.-, Ra Noger R.
                                                                                                                                                                                                                                                                                                       MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stappleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                           Systematic review.",
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

that serves as a template for the assembly of the suprestructure (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable multisynthetase ORFNames=CG12304;
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25-JAN-2005
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                                                                                                                                                                                                                                                                        "Annotation of the Drosophila melanogaster euchromatic
                                                                                                                                                                                                                                                                                                 Lewis S.E.;
  SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl arginyl, and aspartyl-tRNA synthetases as well as three auxi proteins, pl8, p48 and p43 (By similarity).

SIMILARITY: Contains 1 GST-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Last sequence update)
(Rel. 46, Last annotation updat
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Zhao Q., Zheng L.,
Zhu X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p38
                                                     three auxiliary
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K.A.,

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Best Local S
Matches 85
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IntAct; Q9VUR3; -.
FlyBase; FBgn0036515; CG12304.
InterPro; IPR010987; GST_Clike.
InterPro; IPR0404046; GST_Cterm.
Pfam; PF00043; GST_C; 1.
Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
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Local Similarity 25.6%;
hes 85; Conservative 50
                                                                 291
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                                                                                                                                                                                                           SV-----PENILKCFGEQNKKQPRQDYQLGFTILIWKNVPKTQMKFSIQTMCPIEGEGN
                                                                                                                                                                                                                                                                                                                                          GGSQMSVADVGVYSSL----IRMPAVTEK 315
                                                                                             AGNELTVADVVLWSVLQQIGGCSVTVPANVQR 301
                                                                                                                           IIRYLGRVGPAEYRYEGSPLCNEIDLVLDICYQLLRCNTHKTQVAMVRLLDKRLQKQQYF
                                                                                                                                                           IARFLFSLFGQKHNAVNATL---IDSWVDIAIFQLKEGSSKEKAAVFRSMNSALGKSPWL 269
                                                                                                                                                                                          DIGPAAREFEANLAKV--PVNPALPK----ISVTLIWKNCEHTEMISSPTMYVPIYGEVN
                                                                                                                                                                                                                                                           TAFONG-----GLKEVPLODVVINGHPNFIPYALLALKNAWRNLYTIDVKTFTHSTMA 176
                                                                                                                                                                                                                                                                                         TLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVK 159
                                                                                                                                                                                                                                                                                                                       LGRQIQRLLKDDTASVAARQEKVLKQLEELKAQLGQIR-----AGLGVCG--KTFQHT
                                                                                                                                                                                                                                                                                                                                                                                       IKLPTCMYPLKNVSLAADSLASGSSTSASTSASTSSCKLEANRIDRTGRNAATCALDLDS
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334 AA;
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36933 MW; B68FD70AE621990F CRC64;
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1: geneseqp1990s:*
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8: geneseqp2004s:*
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1758.725 Million cell updates,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	_U	4	w	2	_	Result No.
101	101	101	101	101	101	101	102	103	103	103	104	125.5	125.5	125.5	181	214.5	247	832	1191	1378	1630	1630	1667	1667	Score
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence

is differentially expressed in neuronal tissue

of a first animal

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

101 6.1 1221 5 ABG80321 101 6.1 1221 7 ADD13389 100.5 6.0 1220 6 ABU26069 99.5 6.0 651 2 AAY29614 99.5 6.0 651 2 AAY29621 97.5 5.8 217 7 ADD48150 97.5 5.8 217 7 ADD48150 97.5 5.8 217 7 ADD48154 97.5 5.8 217 7 ADD48154 97.5 5.8 217 7 ADD48154 97.5 5.8 217 7 ADD63084 97.5 5.8 217 7 ADB63084 97.5 5.8 217 7 ADB63088 97.5 5.8 217 7 ADB63088 97.5 5.8 217 7 ADB63088 97.5 5.8 218 2 AAR20033 97.5 5.8 218 2 AAR20033 97.5 5.8 652 5 ABP41869 97 5.8 652 5 ABP41869 97 5.8 525 3 AAY77178 97 5.8 5215 8 ADL91339 97 5.8 5215 8 ADL91339 97 5.8 5215 8 ADL9130	6.1 1221 5 6.1 1221 5 6.0 1220 7 6.0 1220 7 6.0 650 2 5.8 217 7 5.8 218 7 5.8 218 7 5.8 218 7 5.8 5221 4	45	44	43	42	41	40	39	38	37	36	35 5	34	<u>ა</u>	32	31	30	29	28	27	
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26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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Best Local
                                                           WO2004030615-A2
                                                                                                                                                                                        Tumour-associated antigenic target; TAT; human; overexpression; c; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target (TAT) polypeptide PRO81501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM80843 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YÓLGFTLÍMKNYÞKTOMKFSIOTMCFIEGEGNÍARFLFSLFGOKHNÁVNÁTLÍÐSMYÐÍA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DÍVÍNANPÁSÞÞLSLLVLHRLLCEHFRVLSTVHTHSSVKSVÞENLLKCFGEQNKKQÞRQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPMYQVKÞÝHGGGÁÞLRVELÞTCMÝRLÞNVHGRSYGÞÁÞGÁGHVQEESNLSLQÁLESRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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Pred. No. 5.
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5.4e-167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus mammals. The invention also relates to nucleic acid and polypeptide compared to neguence as effective teargets for the diagnosis and treatment of cancer in compared to the TAT nucleic acid and polypeptide compared to the TAT nucleic acids and compared to the TAT nucleic acids and polypeptide and antibody specific for a TAT polypeptide; a peptide or organic composition; and methods and compositions for the treatment or compositions of cancer in mammals. TAT polypeptide, a peptide or organic compositions of cancer in mammals. TAT polypeptide, are useful concreased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder, colorectal cancer, melanoma and leukaemia. TAT mucleic acids may further be chromosome identification and in gene therapy. The present sequence and corposents a TAT polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12;
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                                                                                                                                                                                                                                                             61 DILKRLYELKAAVDGLSKMIQTFDADLDVTNIIQADEFTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                                                                                                                             320;
                                                                                                                                                                                                                                                                                                                      1 MPMYQVKPYHGGGAPLRVELPTCMYRLFNVHGRSYGPAPGAGHVQBESNLSLQALESRQD
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                    RWMRSCENLAPFNTALKLLK 320
                                                                                                                             YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                      IFQLKEGSSKEKAAVFRSMNSALGKS
                                                                   IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ 300
                                                                                                                                                                        DIVINANPÁSPPLSILVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                                                                                                                   DIVINANPASPELSILVLHRLLCEHFRYLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                                                                                                                                                     DILKRLYBLKAAVDGLSKMIQTPDADLDVTNIIQADBPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                                                  MPMYQVKPYHGGGAPĹŔVĖĹPTĊMYRĹPNVHGRSYGPAPGAGHVQEĖSNĹSĹQAĹESRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2179; 7273pp; English
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 5
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                                             PWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
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Matches 312
                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is JTV1 protein and is encoded by DNA isolated from human chromosome 7. The JTV1 coding sequence is located upstream from hPMS2. JTV1 cDNA can be used as probes to detect chromosome 7 deletions involving JTV1. Due to the overlapping promoter regions, deletions of JTV1 would also affect PMS2 (a mismatch repair gene) expression, leading to hereditary non-polyposis colorectal cancer. JTV1 can also be used to assay activity or competence of the PMS2 promoter region, the presence of JTV1 suggesting that the PMS2 promoter is intact. JTV1 sequences can also
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel chromosome 7 gene, JTV1 - used f deletions, and PMS2 promoter activity.
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mismatch repair gene; hereditary non-polyposis colorectal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologous recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1997
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                                                                                                                                                                                                                                                                                           MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                  RWMRSCENLAPF
                                                                                                                           YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                                                                                                                                                                                    DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                   DILKRLYELKAAVDGLSKMIQTFDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
RWMRSCENLAPF 312
                                                     I FQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
                                                                                                           YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                                                                                                                                DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                                                                                                                                                                                          MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 2; 31pp; English
                                                                                I FOLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
                                                                                                                                                                                                                                                                                                                                                                                                                 guide homologous recombination at the PMS2 lccus
                                                                                                                                                                                                                                                                                                                              97.8%; So llarity 100.0%; I Conservative 0;
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Pred. No. 4.3e-163;
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                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
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DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK

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                                                                                                                                                                                                                                                                                               The present invention relates to an isolated p38/JTV-1 protein for use as comedicament. The p38/JTV-1 protein or the pharmaceutical composition is cuseful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, lead or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, common, certical cancer, sallopian tube carcinoma, certical cancer, small cancer, vaginal carcinoma, chodgkin's disease, esophageal cancer, vulval cancer, vaginal carcinoma, cusefundary, thyroid cancer, parathyroid cancer, small intestine cancer, soft tissue cumour, urethral cancer, parathyroid cancer, stonest, soft tissue cumour, urethral cancer, parathyroid cancer, kidney cancer, chronic or acute cutemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary component components components of the protein is useful as a target for carcering new anticarer acret a femour accuser accusers and target for carcering new anticarer accusers for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target for the protein is useful as a target and the protein is useful as a target and the protein is 
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Matches 312;
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                                                                                                                                                                                                           Sequence 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-627822/61.
N-PSDB; ADR86548.
                                                                                                                                                                                                                                                   screening new anticancer agents. The present sequence represents 312 amino acid sequence of p38/JTV-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAR-2003; 2003KR-00013058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-SEP-2003; 2003EP-00020344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-312 amino acid sequence of p38/JTV-1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticancer agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; SEQ ID NO 4; 47pp; English.
                                                   1 MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                  Similarity
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MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                       Conservative
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                                                                                                                            97.8%; Score 1630; DB 8; 100.0%; Pred. No. 4.3e-163;
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06-JUN 2001; 2001US-0296418P
07-JUN-2001; 2001US-029575P
11-JUN-2001; 2001US-029575P
12-JUN-2001; 2001US-029573P
12-JUN-2001; 2001US-029528P
15-JUN-2001; 2001US-0299528P
16-JUN-2001; 2001US-0299399
19-JUN-2001; 2001US-0299399
20-JUN-2001; 2001US-0299399
20-JUN-2001; 2001US-0300883P
20-JUN-2001; 2001US-0300839
20-JUN-2001; 2001US-030177P
26-JUN-2001; 2001US-0301890P
28-JUN-2001; 2001US-0301890P
28-JUN-2001; 2001US-0301890P
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28-JUN-2001; 2001US-0301890P
28-JUN-2001; 2001US-0301890P
29-JUN-2001; 2001US-0301890P
29-SEP-2001; 2001US-03391297P
29-SEP-2001; 2001US-03391297P
20-JUN-2001; 2001US-0339129P
20-FEB-2002; 2002US-035912P
20-FEB-2002; 2002US-0359035P
20-FEB-2002; 2002US-0359034P
20-FEB-2002; 2002US-0359034P
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20-FEB-2002; 2002US-0359034P
20-FEB-2002; 2002US-0359034P
20-FEB-2002; 2002US-0359044P
20-FEB-2002; 2002US-0359044P
20-FEB-2002; 2002US-035944P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oyuseant; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping, there there are the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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2001US-0296404P.
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ADR86553;

ADR86553

standard;

protein;

229

84-312 amino acid sequence of p38/JTV-1 protein.
p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.

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Best Local S
Matches 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E; Dipippo VA, Edinger SR, Elsen A, Ellerman K, Gangolli EA; Dipippo VA, Edinger SR, Elsen A, Ellerman K, Gangolli EA; Gerlach VI., Gorman L, Gou X, Herrmann JI., Hjalt T, Ji W, Kekuda I Gerlach VI., Gorman L, Gou X, Herrmann JI., Hjalt T, Ji W, Kekuda I Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I; Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I, Rieger DK; Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK; Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO
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DB; ADC10203.
245
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                  LQQIGGCSVTVPANVQRWMRSCENLAPF
                                                                                          HNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSV
                                                                                                                                                                LLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQK
                                                                                                                                                                                                                                      ALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPEN
                                                                                                                                                                                                                                                                                                                  QEESNLSLQALESRQDDILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTN
LOQIGGCSVTVPANVQRWMRSCENLAPF
                                                                       HNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSV
                                                                                                                                             LLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQK
                                                                                                                                                                                                                   ALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPEN
                                                                                                                                                                                                                                                                                         QEESNLSLQALESRQDDILKRLYELKAAVDGLSKMIQTPDADLDVINIIQADEPTTLTIN
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; Pred. No. 1.6e-136;
0; Mismatches 0;
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272
                                   312
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RESULT 7
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AC ADR8
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AC ADR8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to an isolated p38/JTV-1 protein for use as CC medicament. The p38/JTV-1 protein or the pharmaceutical composition is CC useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cC cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, cC endometrial cancer, saal cancer, colon cancer, fallopian tube carcinoma, cC endometrial carcinoma, cervical cancer, swill cancer, vaginal carcinoma, CC endometrial cancer, parathyroid cancer, small intestine cancer, soft tissue cumour, urethral cancer, parathyroid cancer, small intestine cancer, soft tissue CC leukemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC concer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC concer, pancer agents. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 84-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                 18-NOV-2004
                                                  ADR86552;
                                                                                ADR86552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
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                                                                                                                                                                                                                                                         MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                                                                    EHFRYLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLINKNVPKTQMKFSIQT
                                                                                                                                                                                                                                                                                                                             EHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQT
                                                                                                                                                                                                                                                                                                                                                                                                      DADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6; 47pp; English.
                                                                                                                                                                                                                                    MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                                                                                                                                       DADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPNSPPLSLLVLHRLLC
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                 (first entry)
                                                                                protein; 161
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Pred. No. 7.2e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT 8
ABP01502
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AC ABP0
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AX

ABP01502 standard;

protein;

51 ₿

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24-JUN-2002 ABP01502;

(first entry)

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                                                                                                                                                                                                                                                                                                                                            The present invention relates to an isolated p38/JTV-1 protein for use as CC medicament. The p38/JTV-1 protein or the pharmaceutical composition is CC useful as medicament for treating breast cancer, large intestinal cancer, CC lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, CC cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, cC endometrial carcinoma, cervical cancer, fallopian tube carcinoma, CC endometrial cancer, colon cancer, small intestine cancer, endocrine CC loukemia, thyroid cancer, parathyroid cancer, small intestine cancer, soft tissue cumour, urethral cancer, parathyroid cancer, adrenal cancer, soft tissue CC loukemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter CC cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC adenoma, or their combination. The protein is useful as a target for Screening new anticancer agents. The protein is useful as a target for 1 cancer.
                                                                                                                                                                                                                                Query Match
Best Local S
Matches 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated {\tt p38/JTV-1} protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
                                                                                                                                                                                                                                                                                                              Sequence 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-2003; 2003KR-00013058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-SEP-2003; 2003EP-00020344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-161 amino acid sequence of p38/JTV-1 protein
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                                                                                                                                                                                                                                                   Local Similarity
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                                  121
                                                                         61
                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; SEQ ID NO 5; 47pp; English
                                                                                                                                                                         1 MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                    DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV 161
                                                                                                    DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                   MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                       DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV
                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                49.9%; Score 832; DB 8;
100.0%; Pred. No. 3.9e-79;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                     Length 161;
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161
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The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 or the specification). ABM15762 to ABM27252 encode the human ORFX or the proteins given in ABM15762 to ABM27252 encode the human ORFX CC proteins given in ABM00010 to ABM15010. ORFX proteins are useful for creating or preventing a pathology associated with an ORFX-associated of controlled with ORFX-associated with an ORFX sequences can be used in gene therapy. ORFX sequences can be used in the controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled contro
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Best Local
                                                                                                                                                                                                       Sequence 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2986; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2001; 2001WO-US010B36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX protein sequence
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                              \vdash
                                                                                                                    49;
                                                                                                                                    Similarity
                                         DGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVI 124
             DGLSKMIHTPDADLDVTNILQADEPTTLTTNALDLNSVLGKDYGALKDÍVÍ
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                                                                                                   Score 247; DB Pred. No. 4.5e 1; Mismatches
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                                                                                                                             DB 5;
.5e-18;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0140-ABL16175) and the encoded proteins (ABB57737-BB7272). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                               Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 14196; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
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                                                                                                                                                                                                                                                                    18 VELPTCMYRLPNY----HGRSYGPAPGAGHVQEESNLSLQA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Drosophila and
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AGNELTVADVVLWSVLQQIGGCSVTVPANVQR 301
                                                                                                                                                                                                                                                                                                                         Similarity
                                               IARFLFSLFGQKHNAVNATL---IDSWVDIAIFQLKEGSSKEKAAVFRSMNSALGKSPWL
                                                                           DIGPAAREFEANLAKV--PVNPALPK----ISVTLIWKNCEHTEMISSPTMYVPIYGEVN
                      I IRYLGRVGPAEYRYEGSPLCNEIDLVLDICYQLLRCNTHKTQVAMVRLLDKRLQKQQYF
                                                                                                    SV-----PENILKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGN
                                                                                                                               TAFQNG------GLKEVPLQDVVINGHPNFIPYALLALKNAWRNLYTIDVKTFTHSTMA 176
                                                                                                                                                           TLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVK 159
                                                                                                                                                                                       LGRQIQRLLKDDTASVAARQEKVLKQLEELKAQLGQIR-----
                                                                                                                                                                                                                ------LESRQDDILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPT
                                                                                                                                                                                                                                          IKLPTCMYPLKNVSLAADSLASGSSTSASTSASTSSCKLEANRIDRTGRNAATCALDLDS
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2000US-00614150
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Match
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
   BLOSUM62
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1667
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             GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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          US-09-949-016-11312
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US-09-143-184-48
US-09-156-317-10
US-09-105-537-2
US-09-105-537-2
US-09-105-537-2
US-09-105-632-1
US-09-105-632-1
US-09-105-632-1
US-09-105-632-1
US-09-540-824-2
US-09-540-824-2
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US-09-540-824-2
US-09-38-092-736
US-09-949-016-11178
US-09-976-239-2
US-09-976-239-2
US-09-976-239-2
US-09-976-239-3
US-09-976-239-3
US-09-976-239-3
US-09-976-239-3
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US-09-112-710-13
US-09-128-779B-4
US-09-138-352-6834
US-09-134-001C-4904
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Sequence 11312, A
Sequence 2, Appli
Sequence 48, Appli
Sequence 4, Appli
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85.5 5.1 1440 3 US-09-357-351-37 Sequence 37, 9	B	US-	
## Patent No. 5194 9-357-251-37 9-357-251-37 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-611-2 8-406-549-2 8-446-2 8-446-2 8-4	hery Mert Lo	Sequence seq	
## Patent No. 5194 9-357-251-37 9-357-251-37 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-611-2 8-406-549-2 8-446-2 8-446-2 8-4	1 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 22 Kg 24 Kg 2	-016-11 NO. 681 NO. 681 NO. 681 NO. 681 NO. 10	N 44444WW 0
## Patent No. 5194 9-357-251-37 9-357-251-37 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-611-2 8-406-549-2 8-446-2 8-446-2 8-4	CONSET CONSET CONSET MYQVKPY 	, Appli Aprion: Aprion: Aprion: NATION: NATION: NATION: OG DATE: OG DATE: OF TOTAL OF	
## Patent No. 5194 9-357-251-37 9-357-251-37 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-611-2 8-406-549-2 8-446-2 8-446-2 8-4	100. 100. 100. 100. 100. 100. 100. 100.	Cation Craig POTYMOP WITH 1 1307 1307 2000- 000-10- 000-10- 000-10- 000-10- 000-000-	1365 1440 1559 1135 829 829 829 829 829 829 829 829 829 829
## Patent No. 5194 9-357-251-37 9-357-251-37 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-537A-97 8-409-611-2 8-406-549-2 8-446-2 8-446-2 8-4	.RVE	US/ PHI UMA 10MA 10MA 10MA 10MA 10MA 10MA 10MA 10	
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NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 0110

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.8
Best Local Similarity 100.
Matches 312; Conservative
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US-08-518-862C-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Nicolaides, Nicholas C.
TITLE OF INVENTION: Human JTV1 Gene Overlaps PMS2 Gene
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APPLICATION NUMBER: US/08/518,862C
FILING DATE: 24-AUG-1995
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
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5: 5843757
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                       RWMRSCENLAPF 312
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100.0%; Pred. No. 3.5e-177;
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US-08-...

Sequence 10, 5849894

Patent No. 5849894

GENERAL INFORMATION:

APPLICANT: Clemente, Thomas b.

APPLICANT: Mitsky, Timothy A.

APPLICANT: Mitsky, Timothy A.

APPLICANT: Stark, David M.

TITLE OF INVENTION: Improved Rhodospirillum Rubrum

INUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-756-317-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/443,184A
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
SEQ ID NO 48
LENGTH: 1512
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Marches 45; Conserva
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COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: FOR PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cunningham, Mary Jane
APPLICANT: Zweiger, Gary
APPLICANT: Kaser, Matthew R.
APPLICANT: Banzer, Scott
APPLICANT: Beilhammer, Jeffrey J.
APPLICANT: Beilhammer, Jeffrey J.
APPLICANT: Baughn, Mariah
APPLICANT: Baughn, Mariah
APPLICANT: Azimzai, Yalda
APPLICANT: Lai, Preeti
TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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SUMMARIES
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1630 1191 832 102 101 101 101 101 101 100.5 100.5 97.5	Score
97.8 491.4 69.9 66.1 56.6 6.1 1	Query Match Length DB
312 229 161 201 826 833 1221 1221 1221 1221 1221 1221 1221	Length
16 16 16 10 10 10 15 15 15	BG
US-10-463-676-4 US-10-463-676-5 US-10-463-676-5 US-10-369-493-13717 US-09-746-660A-92 US-09-746-660A-90 US-09-919-891-2 US-09-738-626-5163 US-10-450-055-2 US-10-494-675-156 US-10-425-114-58897 US-10-282-122A-53993 US-10-264-049-3001	ID
Sequence 4, Appli Sequence 6, Appli Sequence 5, Appli Sequence 13717, A Sequence 92, Appl Sequence 2, Appli Sequence 2, Appli Sequence 5163, Ap Sequence 2, Appli Sequence 25, Appli Sequence 58897, A Sequence 53993, A Sequence 3001, Ap	Description

1644	62-122A-		ហ ហ ហ	91.5	4 4 5 4
3838	US-10-282-122	1206	າ ທ	92	43
-251522	US-10-424-599		•	92	42
3766	US-10-424-599		•	93.5	41
3904	US-10-437-963-		•	93.5	40
136277	US-10-437-963		•	94	9
-260388	US-10-424-599-		•	94	38
4	US-10-369-493			94	37
912	US-10-28		•	94.5	36
2	US-10-032-		•	95	35
013	US-10-369-493-10		•	95	34
	US-10-914-244-		•	95	33
	US-10-252-518-		5.7	95	32
	US-10-266-787-		•	95	31
	14 US-10-259-632-1	559	•	95	30
	US-10-218		5.7	95	29
	US-09-820-	559	•	95	28
	9 US-09-821-016-1	559	•	95	27
2633	15 US-10-425-114-42		5.7	95.5	26
115189	US-10-437-963-1		•	96	25
	-10-655-799-		5.8	96.5	24
3870	US-10-437-		•	96.5	23
	US-10-271-889-		•	97	22
	US-09-836-821-			97	21
	0 US-09-988-38	5215	•	97	20
	8-60-Sn	5215	•	97	19
	US-09-861-289-	5215		97	18
	9 US-09-364-847-35	856	•	97	17
	US-09-364-847-3	856	•	97	16
	US-09	559		97	15
6483	16 US-10-437-963-175483	711	5.8	97.5	14

ALIGNMENTS

RESULT 1 US-10-463-676-4

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; NAME/KEY: PEPTIDE
; LOCATION: (1)...(312)
; OTHER INFORMATION: 1-312 amino acid sequence of p38/JTV-1
uS-10-463-676-4
                         S
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Method for Treating Cancer Using p38/JTV-1 and Method
TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating Cancer
FILE REFERENCE: 012679-091
CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 17
SOFTMARE: FastSEQ for Windows Version 4.0
LENGTH: 312
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10463676 Publication No. US20040175375A1 GENERAL INFORMATION:
                                                                                                                                                                       Query Match 97.8%; Score 1630; DB 16; Length Best Local Similarity 100.0%; Pred. No. 6.4e-153; Matches 312; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kim, Sunghoon APPLICANT: Park, Bum-Joon
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
61 DILKRLYELKAAVDGLSKMIQIPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                         1 MPMYQVKPYHGGGAPLRVELFTCMYRLFNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                             MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                             Indels
                                                                                                                                                                             0
                                                                                                                                                                             Gaps
                                 120
                                                                                8
                                                                                                                              60
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Sequence 6, Application US/10463676

Publication No. US20040175375A1

GENERAL INFORMATION:
APPLICANT: Kim, Sunghoon
APPLICANT: Kim, Sunghoon
APPLICANT: Moreover for Treating Cancer Using P38/JTV-1 and Method
TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
TITLE OF INVENTION: Moreover for Treating Cancer Using P38/JTV-1 and Method
TITLE OF INVENTION UNMBER: US/10/463,676
CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR APPLICATION NUMBER: KR 50-2003-13058
INUMBER OF SEQ ID NOS: 17
SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 6
IFNORTH: 720
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US-10-463-676-5
Sequence 5, Application US/10463676
Publication No. US20040175375A1
GENERAL INFORMATION:
APPLICANT: Kim, Sunghoon
APPLICANT: Park, Bum-Joon
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US-10-463-676-6
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                                                                                                                RESULT 3
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LOCATION: (1)...(229)
OTHER INFORMATION: 84-312 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 229
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                                                                                                                                                                                                     264
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                                                                                                                                                                   GKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQRWMRSCENLAPF
                                                                                                                                                                                                                                            MCPI EGEGNIAR FLFSLFGQKHNAVNATLI DSWVDI AI FQLKEGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                                                MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                                                                                  EHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQT
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; NAME/KEY: PEPTIDE
; LOCATION: (1)...(161)
; OTHER INFORMATION: 1-161 amino acid sequence of p38/JTV-1
US-10-463-676-5
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Best Local S
Matches 161
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13717
LENGTH: 201
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13717, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                        Matches
                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FRACEORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating Cancer FILE REFERENCE: 012679-091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                      y Match 6.1%; Score 102; DB 15; Local Similarity 30.5%; Pred. No. 0.17; hes 32; Conservative 15; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                     270
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                                                                                                          GNIARFLFSLFGQKHNAVNA-TLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSALGKSPWL 269
                                                                          GPAAARLITVFGAKFNAEEVITRAHNFLKV---
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AGTEPTIADVSAYSYIAHAPEGNVSLDDYANVRAWLSRIEALPGF
                                AGNELTVADVVLWSVLQQI---GGCSVTVPANVQRWMRSCENLAPF
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                                                                                                                                                                                             Length 201;
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  191
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Minimum DB
Maximum DB
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Maximum Match 10
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1667
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1: pir1:*
2: pir2:*
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4: pir4:*
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hypothetical prote	MAD1 protein - yea	unknown protein (i	translation elonga	methyl-accepting c	glutathione transf	ctp synthase (pyrG	hypothetical prote	multifunctional am	probable magnesium	SEC8 protein - yea	glutathione transf	translation elonga	glutathione transf	conserved hypothet	rho-type GTPase-ac

ALIGNMENTS

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-728 <DAV> A;Cross-references: UNIPROT:O65253; EMBL:AF058914; NID:g3047074; PID:g3047084; GSPDB:GN0 A;Experimental source: cultivar Columbia C;Genetics: probable glutamate-tRNA ligase (EC 6.1.1.17) F21E10.12 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C; Pate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C; Accession: T01200 R; Davidson, S.; Rohlfing, T.; David, M.; O'Brian, D. submitted to the EMBL Data Library, April 1998 A; Description: The sequence of A. thaliana F21E10. A; Reference number: Z14258 A; Accession: T01200 RESULT 2 T01200 probable glutamate-tRNA ligase (EC 6.1.1.17) [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) c; Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004 C; Accession: T5.2043 R; Day, I.S.; Golovkin, M.; Reddy, A.S. Biochim. Biophys. Acta 1399, 219-24, 1998 A; Title: Cloning of the cDNA for glutamyl-tRNA synthetase from Arabidopsis thal A; Reference number: 224836; MUID:9765600; PMID:9765600 A; Accession: T5.2043 Ś A;Cross-references: UNIPROT:082462; EMBL;AF067773; PIDN:AAC36469.1 C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology C;Keywords: ligase A;Status: preliminary; translated from A;Molecule type: mRNA A;Residues: 1-719 <DAY> 밁 용 Ś Matches Query Match Local 247 GSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLMSVLQQIGGCSVTVPANVQRW 302 188 IWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA-IFQLKE 128 PASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTL 94 56 LLRYV------GRSAKKLPDFYG--NNAFDSSQIDEWVDYASVF--SS 48; Similarity GSEFENAC--GRVDKYLESSTFLVGHSLSIADVAIWSALAGTG------QRW PESPPLSVIVALSLSASPV----TIDSSAAATTVPSFV---FSDGRKLN-----GATV Conservative 7.5%; 26; Score 125.5; DB 2; Pred. No. 0.017; Mismatches GB/EMBL/DDBJ 53; Indels Length 719; Arabidopsis thaliana 49; Gaps 246 5 187 9

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glutathione transferase (EC 2.5.1.18) yb3 - C:Species: Rattus norvegicus (Norway rat) C:Date: 28-Dec-1987 #sequence_revision 28-Dec. C:Accession: A29036 R;Abramovitz, M.; Listowsky, I. J. Biol. Chem. 262, 7770-7773, 1987 A;Title: Selective expression of a unique gl.
                                                                                                                      RESULT
A29036
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C; Superfamily. h.
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; I chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio che A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82441
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
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A;Map position: 5
A;Map position: 5
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase ho C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis F;223-499/Domain: glutamine-tRNA ligase homology <EGL>
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22; Mismatches
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      glutathione
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H.; Dragoi, I.;
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A;Molecule type: mRNA
A;Residues: 1-645 <VALD-
A;Residues: 1-645 <VALD-
A;Residues: 1-645 <VALD-
A;Residues: GB:U78524; NID:g1696006; PIDN:AAB58488.1; PID:g1696007
A;Note: it is uncertain whether Met-4 or Met-6 is the initiator
C;Comment: This protein is localized to the nucleus and interacts with Gu/RNA
C;Keywords: phosphoprotein
F;50-59/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;362-374/Region: nuclear location signal F;514-517,551-554,592-595,606-609/Region: 4-residue repeats (N-T-S-L) F;714-517,551-554,592-595,606-609/Region: 4-residue repeats (N-T-S-L) F;7,177,322,412,432,460,461,462,470,614,627/Binding site: phosphate (Thr) (covalent) #status predict
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A.Title: Cloning and characterization of Gu/RH-II binding prod. Reference number: JC5517; MUID:97320420; PMID:9177271
A;Accession: JC5517
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C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C;Accession: JC5517
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C;Superfamily: glutathione transferase
C;Keywords: transferase
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A;Accession: A29036
A;Molecule type: mRNA
A;Residues: 1-218 <ABR>
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                                                                                                                                                                                                                                                                                       134 ---SLL-VLHRLLCEHF-RVLSTVHTHSSVKSVP----ENLLK--CFGEQNKKQ----
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                                                                                                                                          FAFALTPQQVQQISSSM----DISGTKCDFTVQVQLRFCLSETSCPQEDHFPPNLCVKVNT 219
                                                                                                                                                                                                                                      LPVSLLGPKHELELPHLTSALHPVHPDIKLQKLPFYDLLDELIKPTSLASDNSQRFRETC 162
                                              KPCSLPGYLPPTKNGVEPKRPSRPINITSLV-----RLSTTVPNTIVVSWTABIGRNYSM
                                                                                                                                                                                           -----PRODYQLGFTLIWKNVPKTQMKFSIQ-----TMCPIEGEG-----
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1 brachydanio
4 brachydanio
5 vibrio chol
1 mus musculu
2 anopheles 9
5 drosophila
6 drosophila
2 drosophila
3 drosophila
3 drosophila
4 drosophila
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6 drosophila
7 homo sapien
7 corynebacte
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9 drosophila
1 drosophila
1 drosophila
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RESULT RESULT	
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Matches 320
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InterPro; IPR094046; GST Cterm.
Pfam; PF004043; GST C; 1.
Protein biosynthesis.
SEQUENCE 320 AA; 35349 MW;
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EMBL; BC010156; AAH10156.1; --
EMBL; AF116615; AAF71039.1; --
H-InvDB; HIX0006460; --
MIM; 600859; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W.,
Lee S.W., Han J.M., Lee H.-W., Kim S.,
"Downregulation of FUSE-binding protein and c-myc by tRNA synthetase coffactor p38 is required for lung cell differentiation.";
"Downregulation of FUSE-binding protein and c-myc by tRNA synthetase coffactor p38 is required for lung cell differentiation.";
"Downregulation of FUSE-binding protein and c-myc by tRNA synthetase coffactor p38 is required for lung cell differentiation.";
-I-FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure. Mediates ubiquitination of FUBP1 and its degradation b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
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SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxil proteins, p18, p48 and p43. Binds FUBP1.

SIMILARITY: Contains 1 GST-like domain.

CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 312.
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                                                                                                                       RWMRSCENLAPFNTALKLLK 320
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                                                                                                RWMRSCENLAPFNTALKLLK
                                                                                                                                                                                IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
                                                                                                                                                                                                                               YÓLGFTLIWKNYÞKTÓMKFSIÖTMCÞIEGEGNIARFLFSLFGOKHNAVNÁTLIDSWYDIA
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           PRELIMINARY;
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           PRT;
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RA KITALUSE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA KITALUSE R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Halting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
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Best Local
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InterPro; IPR004046; GST Cterm.
InterPro; IPR001987; GST C_like.
Pfam; PF00043; GST C; 1.
SEQUENCE 320 AA; 35335 MW; 19F14BF758612E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krzywinski "..., ...., Jones S.J., Marra M.A.; Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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TISSUE=Placenta;
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TISSUE=Placenta;
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Mammalia; Eutheria;
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Pred. No. 1.3e-126;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altechul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wanng J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wanng J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Hopkins R.F., Jordan H., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., William T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., William R., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hiltalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hilting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hilting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hilting M., Wadan A., Schaman J.W., Green E.D., Dickson M.C.,

B A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-FVB/N-3; TISSUE-Mammary tumor;
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Mammalia; Eutheria;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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InterPro; IPRO10987; GST_C like.
Pfam; PP00043; GST_C; 1.
SEQUENCE 320 AA; 35396 MW; 1
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                                                                                                                           DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPEN:JKCFGEQNKKQPRQD
                                                                                                                                                                                                           DILKRLYELKAAVDGLSKMIHTEDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
                                                                                                                                                                                                                                             DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                                                                                                               MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
YQLGFTLIWKNVPKTQMKPSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                                                            DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHE
                                                                                                                                                                                                                                                                                                                                MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
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TISSUE=Mammary tumor.
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87.2%;
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Pred. No. 1.
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CONTRAINSCAECH II; TISSUE-Mammary tumor;

REDININE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altausner R.D., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Scheetz T.B.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Scheetz T.B.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Walin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon B., Ketteman M., Madan A., Golbs R.A.,

RA Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,
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Best Local S
Matches 279
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01-JUN-2002
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Mammalia; Eutheria;
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Name=Jtvl;
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FEAM; PF00043; GST_C; 1.
FEAM; PF0043; GST_C; 1.
FEQUENCE 320 AA; 35423 MW; 1
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DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                       DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
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l. Acad. Sci. U.S
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InterPro; IPR010987; GST_C like.
InterPro; IPR01046; GST_Cterm.
Pfam; PF00043; GST_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99096915; PubMed=9878398; DOI=10.1006/jmbi.1998.2316; Quevillon S., Robinson J.-C., Berthonneau E., Siatecka M., Mirande "Macromolecular assemblage of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last amoutation update)
Multisynthetase complex auxiliary component p.
Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Verte)
Mammalia, Eutheria, Rodentia, Sciurognathi, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure.

SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutawyl prolyf-tRNA synthetase, the monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43.

SIMILARITY: Contains 1 GST-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Biol. 285:183-195(1999).
FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecul.
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                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                            biosynthesis.
E 320 AA; 3
DILKRLYELKAAVDGLSKMIQTFDADLDVTNIIQADEFTTLTTNALDLNSVLGKDYGALK
                                                                                                                    MEMYQVKEYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQBESNLSLQALESRQD
                                                                             MPMYQVKSYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
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Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                          Score 1444; DB 1;
Pred. No. 7.6e-109;
6; Mismatches 27;
                                                                                                                                                                                                                                                                                                   6D24E033ABEC810A CRC64;
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RESULT 6

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               Query Match
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Matches 243;
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RX MEDLINE=22388257; PubMed=12477932; DOI=0.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=0.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulahy S.J.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.",

REL Proc. Natl. Acad Sci II S a 94.16800_15001
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MGD; MGI:2385237; Jtv1.

InterPro; IPR004046; GST Cterm.

InterPro; IPR010987; GST C 11ke.
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Q8R3V2;
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01-JUN-2002
01-OCT-2003
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                        tted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
BC024480; AAH24480.1; -.
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TISSUE=Mammary tumor.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
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Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ
EMBL; BC074561; AAH74561.1; -.
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Xenopodinae; Xenopus.
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FEAM; PP00043; GST_C; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                         Local Similarity
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                         68.7%; Score 1144.5; DB 2; Length 311; 68.8%; Pred. No. 1.5e-84;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischall S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Barownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S. J. Marra M.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGC80304 protein.
Name=MGC80304;
                                                                                                                                                                                                                                                                                                                                                                                       Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,0
and mouse CDMA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                              "Genetic and genomic tools for
                                                                                                                                                                                                                                WEDLINE=22341132;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                            225:384-391 (2002)
                                                                                                                                                                                           1132; PubMed=12454917;
Strausberg R.L., Wagne
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                                                                                                                                                                                           Wagner
                                                                                                                      Xenopus
                                                                                                                                                                                                DOI=10.1002/dvdy.10174;
C., Pontius J., Clifton S.W.,
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                                                                                                                      research: The NIH Xenopus
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A MEDLINE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Holards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Submitted (JUN-2004) to the EMBL/G
EMBL; BC072178; AAH72178.1; -.
InterPro; IPR004046; GST_C_term.
InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
SEQUENCE 311 AA; 34424 MW; D5E
                                                                                                                                                                                                                                                                                                                                           Jtv1-prov protein.

Kenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM
TISSUE=Embryo;
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01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Q7ZYD7;
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Pred. No. 3.8
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Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/G
EMBL; BC043832; AAH43832.1; -.
InterPro; IPR004046; GST_C_Clike.
InterPro; IPR010987; GST_C_1ke.
Pfam; PF00043; GST_C; 1.
SEQUENCE 311 AA; 34647 MW; 2F0
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22341132; PubMed=12454917; |
Klein S.L., Strausberg R.L., Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Generation and initial analysis and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99: [2]
                                                                                                                                                                                                                                                                                                                                                                                     "Genetic
                                                                                                                                                                                                                                                                                                                                     ISSUE=Embryo;
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           RWMRSCENLAPFNTALKLLK 320
                                    KWMKSCENLASFKSVLRFLK
                                                                     YQLGFTLIWKDVPKPQMKFSIQNMCPIBGBGNIGRFLFSLFGYKFNAVNATLIDGWVDTA
                                                                                  YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                                                                                                              DILKRLYELKAAVDGLSKMIQTFDADLDVTNIIQADEFTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                               MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
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                                KEKAAVLKAMNTTLGKSPWLVGNELTVADIVSWCAVQQCGN-STVVPPNVQ
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Pred. No. 1.4e
39; Mismatches
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311
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r L., Pontius J., Clifton
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1.4e-83;
es 51;
                                                                                                                                                                                                                                                                                                                                                                                research: The NIH Xenopus
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Zgc:63976, ORFNames=zgc:63976; Brachydanio rerio (Zebrafish) () Bukaryota; Metazoa; Chordata; C Actinopterygii; Neopterygii; Te Cyprinidae; Danio. SEQUENCE FROM N.A.

TISSUB-Kidney;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. Q7T3C0; Q7T3C0; 01-OCT-2003 01-OCT-2003 01-MAR-2004 NCBI_TaxID=7955; (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. PRELIMINARY; 25,00 , Created) , Last sequence upo , Last annotation :) (Danio rerio). ; Craniata; Vertebrata; Buteleostomi; Teleostei; Ostariophysi; Cypriniformes; PRT; 321 ₽ update) update)

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Matches 184; Conser
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Strauberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053178; AAH53178.1; -.
ZFIN; ZDB-GENE-0,04026-2652; zgc:63976.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C like.
Pfam; PP00043; GST_C; 12
SEQUENCE 321 AA; 34852 MW; BA8F6B951208244A CRC64;
                                                                                          Q7Q7A3 PRELIMINARY; PRT; 340 AA. 07Q7A3; 01-MAR-2004 (TrEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last sequence up 01-MAR-2004 (TrEMBLrel. 26, Last annotation AgCP5808 (Fragment).
Name-sgCG50514; ORFNames=ENSANGG00000011827;
 SEQUENCE FROM N.A
                           Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neopeora; Endopterygota; Diptera; Nematocera; Culic
NCBI_TaxID=180454;
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"Generation and initial analysis of more than 15,000 full-length human
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Pred. No. 1.
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                                               Culicoidea;
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RESULT 12
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MEDINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Che, Gabor G.L., A Bark., Deaxeer E.G., Helt G., Nelson C.R., Gabor G.L., A Bark., Denser P.J., Andrews-Pfannkoch C., Baldwin D., A Ballew R.M., Basu A., Barkendale J., Bayraktaroglu L., Beasley E.M., Bellew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., A Baltis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burkis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burkis K.C., Susam D.A., Butler H., Cadieu E., Center A., Chandra I., A Gerson K.J., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabriellan A.E., Garg N.S., Gebart W.M., Glasser K., A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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Best Local Sim
Matches 100;
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PRELIMINARY;

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T 05-JUL-2004 (TrEMBLrel. 27, Created)

T 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

T 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 AA;
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29.2%; Pred.
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RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McNulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradding A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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InterPro; IPR004046; GST Cterm.
InterPro; IPR001987; GST Cc_like.
Pfam; PF00043; GST C; 1.
SEQUENCE 301 AA; 33241 MW; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,

settencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                               FlyBase;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                          FlyBase;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Ventex B. M., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller B., Capatel S., Frise E., Wheeler D.A., Lewis S.E., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The transposable elements of the Drosophila melanogaster euchromatin
a genomics perspective.";
Jenome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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                                                         Similarity
                                                                                                                                                                                                                              (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                  (SEP-2002)
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                          13.4%; Score 224; DB 2; 28.1%; Pred. No. 7.6e-10; tive 47; Mismatches 120
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                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                  35224E17FE03F3BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlson J., S., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                        databases
                                                                  Length 301;
                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Celniker S.;
Submitted (DEC-2003) to the EMBL/G.
EMBL; AY069537; AAL39682.2; -
FlyBase; PB9n0036515; CG12304.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C like.
PF00043; GST_C; 1.
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Q8T060;
01-JUN-2002 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BELGELBY, CARISON OF STAPPLETON, PROBLET N., Agbayani A., Carlson of Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson of Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., F., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., L. Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rub
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
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ORFNames=CG12304;
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FIPYALLALKNAWRNLYTIDVKTFTHSTMADIGPAAREFEANLAKV--PVNPALPK----
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                                      SPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV-----PENLLKCFGEQNKKQPRQDYQ 182
                                                                                                             KAAVDGLSKMIQTEDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPA 129
                                                                                                                                                                           IKLPTCMYPLKNVSLAADSLASGSSTSASTSASTSSCDDTASVAA---ROEKVLKQLEBL
                                                                                                                                                                                                                    VELPTCMYRLPNV------HGRSYGPAPGAGHVQEESNLSLQALESRQDDILKRLYEL
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                                                                                                                                                                                                                                                                                                                                                                        1
313 AA;
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                                                                                                                                                                                                                                                                                                                                                                      34522 MW;
                                                                                                                                                                                                                                                                      13.4%; Score 224; DB 2
28.1%; Pred. No. 8e-10;
tive 47; Mismatches 1
                                                                                          -AGLGVCG--KTFQHTTAFQNG
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era; Muscomorpha;
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LP12114p (Fragment).

Drosophila melanogaster (Fruit fly).

Brosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Rexpetera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Carlson J., Chavez C., Frise E., George R. Park S., Wan K., Yu C., Rubin G.M., Celniker S.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BT012670; AAT08476.1; -.
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                                                                                                                                                                                                                                                                                                           85;
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                                                                                                                                                                                                                                                                                      VELPTCMYRLPNV-----HGRSYGPAPGAGHVQEESNLSLQALESRODDILKRLYEL
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                                                                       EK 303
                                                                                                           CYQLLRCNTHKTQVAMVRLLDKRLQKQQYFGGSQMSVADVGVYSSL-----IRMPAVT
                                                                                                                              AIFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANV
                                                                                                                                                                  LGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATL---IDSWVDI
                                                                                                                                                                                       FIPYALLALKNAWRNLYTIDVKTFTHSTMADIGPAAREFEANLAKV--PVNPALPK----
                                                                                                                                                                                                                             KAQLGQIR-----AGLGVCG--KTFQHTTAFQNG-----GLEEVPLQDVVINGHPN
                                                                                                                                                                                                                                                KAAVDGLSKMIQTPDADLDVINIIQADEPTTLTINALDLNSVLGKUYGALKDIVINANPA 129
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IPR010987; GST_C_like.
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28.1%;
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Last sequence update)
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Pred. No. 8.
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    16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Probable multisynthetase complex auxiliary component p38.
                                                                                                 systematic review.
                                                                                                                       Lewis S.E.;
                                                                                                                                                                                                  GENOME REANNOTATION.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., LiP.W., Hoskins R.A., Galle R.F.,
RA Balder R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burtin G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.C., Rogers Y.H.C., Blazel R.G., Champe M., Ffeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakranglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.
RA Geboson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mouten K.A., Howland T.J., Wein M.-H., Ibegvam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
RA Helson D.R., Nelson K.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Mchulbov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulbov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Naxon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Saunders R.D. C., Scheeler F., Shen H.,
RA Merkulbov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulbov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K., Saunders R.D. C., Scheeler F., Shen H.,
RA Melson D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                            Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
FUNCTION: Probable core protein of the multisynthetase comple that serves as a template for the assembly of the supramolect structure (By similarity).

SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxil proteins, p18, p48 and p43 (By similarity).

SIMILARITY: Contains 1 GST-like domain.
                                                                                                             three auxiliary
                                                                                                                                                                                                                                                                                                                                                        supramolecular
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Search completed: February 23, 2005, 13:57:12 Job time: 61.9811 secs
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Matches 85
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IntAct; OSVUR3; -.
FLYBase; FB9n0036515; CG12304.
InterPro; IPR010987; GST_C_like.
InterPro; IPR004046; GST_Cterm.
Pfam; PF00043; GST_C, 1.
Protein biosynthesTerm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                              213 IARFLFSLFGOKHNAVNATL---IDSWVDIAIFQLKEGSSKEKAAVFRSNNSALGKSPWL
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                                                                                                            ITRYLGRYGPAEYRYEGSPLCNEIDLYLDICYQLLRCNTHKTQVAMYRLLDKRLQKQQYF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                     GGSQMSVADVGVYSSL-----IRMPAVTEK 315
                                                                                                                                                                       DIGPAAREFEANLAKV--PVNPALPK----ISVTLIWKNCEHTEMISSPTMYVPIYGEVN
                                                                                                                                                                                           SV-----PENILKCFGEQNKKQPRQDYQLGFTLIMKNVPKTQMKESIQTMCPIEGEGN 212
                                                                                                                                                                                                                              TAFONG-----GLKEVPLODVVINGHPNFIPYALLALKNAWRNLYTIDVKTFTHSTMA 176
                                                                                                                                                                                                                                                          TLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVK 159
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36933 MW; B68FD70AE621990F CRC64;
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Maximum DB
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Maximum Match 100%
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1758.725 Million cell updates/sec
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Pred. No. score grea and is der d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	s	4.	ω	2	٦	No.	7
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Abm71749 Staphyloc		Abj18952 Pathogen	Abm54677 Propionib	Aau58158 Propionib	Abul6445 Protein e	Aag85046 Shrimp wh	Abm67090 Photorhab	Adn23683 Bacterial	Aam79716 Human pro	Aam78732 Human pro			_		Abg23964 Novel hum	Abb62468 Drosophil	Abp01502 Human ORF	Adr86552 1-161 ami	Adr86553 84-312 am	Ndc10204 Human NOV	Adr86551 1-312 ami	Aaw25776 JTV1 prot	Abm80843 Tumour-as	Human P	Description	

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal

New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.

for

Claim 1; Page; 1017pp; English.

45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28	27	26
93	93	93.5	93.5	•	•	94	95	96	96.5	96.5	٥,	96.5	9	98	98	98	98		98
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559	204	1090	1090	1064	1049	436	722	2273	1440	1440	1440	1398	1398	1032	1016	1013	1004	997	985
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Aar10682	Ads21772	Abg18331	Abg17694	Aae25162	Abb91239	Abb54068	Ads20980			Adp54124	Adn03674	Abm83057	Abm83058	Adn88618	Adn88619	Adn88594	Adn88621	Adn88620	Adn88622
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ALIGNMENTS

RESULT 1
ADE58613
ID ADE5

ADE58613 standard; protein;

320

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29-JAN-2004 ADE58613;

(first entry)

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14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                     Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                 WPI; 2003-268312/26.
GENBANK; Q13155.
                                                                                                                      Woolf C,
                                                                                                                                                                                 14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                               27-FEB-2003.
                                                                                                                                                                                                            WO2003016475-A2
                                                                                                                                                                                                                                                                Human Protein Q13155, SEQ ID NO 4489.
                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                   (FARB
                                                                                                                                         (GEHO)
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                                                                                                                                  GEN HOSPITAL CORP
BAYER AG.
                                                                                                                     D'urso D,
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RESULT 2
ABM80843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc subjected to pain, a method for identifying a compound which regulates cc the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the cc polynucleotides, a method for producing a pharmaceutical composition, a cc method for identifying a compound or small molecule that regulates the cc specification, a method for identifying a compound useful in treating cp polypeptides or their antibodies. The polynucleotide or the treating cc modulates its activity is useful for preparing a medicament for treating cc modulates its activity is useful for preparing a medicament for treating cc injury (CT) and spared nerve injury (Chung), chronic constriction cc injury). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: specification, but was obtained in electronic form directly from WIPO at cr from wire int/win/ininienal nerve amenage.
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Matches 279
                                                                                                                                 Tumour-associated antigenic target; TAT; human; overexpression; c: tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; pincreatic cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                       Tumour-associated antigenic target (TAT) polypeptide PRO81501, SEQ:2179.
                                                                                                                                                                                                                                                                                                                                                      18-NOV-2004
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                                                                                                                          therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ
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87.2%; Pred. No. 7.5e-142;
tive 16; Mismatches 25;
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                                                                                                                                                                                                                                                     cancer;
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WO2004030615-A2

HOMO sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in CC sequences at least 80% identical to the TAT nucleic acid and polypeptide CC polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; apeptide or organic CC molecule which binds to a TAT polypeptide; fusion proteins comprising a CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, and methods and compositions for the treatment or CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful CC increased TAT expression, particularly cancers such as breast cancer, CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central CC used as hybridisation probes, in chromosome and gene mapping, in CC chromosome identification and in gene therapy. The present sequence corporates a TAT polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumor-associated antigenic target polypeptides and nucleic useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; SEQ ID NO 2179; 7273pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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RWLKSCENLAPFSTALQLLK 320
                                                          MFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLMSVLQQTGGSSGAAPTNVQ
                                      IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
                                                                                                                               YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA
                                                                                                                                                                      DÍVÍNANPASPPLSILVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKOPROD 180
                                                                                                                                                                                                                                                           DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
                                                                                                                                                                                             DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVDENLVKCFGBQARKQSRHE
                                                                                                                                                                                                                                         DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                                                                                      MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                                                                            YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFI
                                                                                                                                                                                                                                                                                                           MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 AA;
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Pred. No. 7.5e-142;
6; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 320;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 312 AA;
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mismatch repair gene; hereditary non-polyposis colorectal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Fig 2; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-AUG-1995;
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                                                                                                                                                                                                                DILKRLYELKAAVDGLSKWIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK 120
                                                                                                                                                                                                                                                                      MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                                                                                                                                     MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
            RWLKSCENLAPF 312
                                                                   YQLGFTLIWKWVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA 240
                                                                                                                                                                           DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHE 180
                                                                                                                                                                                                                                  DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
RWMRSCENLAPF 312
                                                                                                                                                             DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
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                                                    I FOLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
                                                                                                        YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
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                                                                                                                                                                                                                                                                                                                                      86.8%;
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                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicolaides NC
                                                                                                                                                                                                                                                                                                                          Score 1436; DB 2;
Pred. No. 5.6e-139;
4; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting chromosome
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DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHE

DIVINANPAS PPLSILVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEONKKOPROD

120 180 180

120

60 0,

13 13 Query Match Best Local Sin Matches 273;

Similarity

86.8%; Sc 87.5%; Pr tive 14;

Score 1436; DB 8; Pred. No. 5.6e-139; 4; Mismatches 25;

Length 312; Indels

0

Gaps

Conservative

1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD

MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD

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                                                                                                                                           The present invention relates to an isolated p38/JTV-1 protein for use as CC medicament. The p38/JTV-1 protein or the pharmaceutical composition is CC useful as medicament for treating breast cancer, large intestinal cancer, CC lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, CC cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, cc rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, CC endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, CC endometrial carcinoma, cervical cancer, small intestine cancer, endocrine cancer, thyroid cancer, penile cancer, small intestine cancer, soft tissue cancer, thyroid cancer, penile cancer, prostate cancer, chronic or acute cumour, urethral cancer, penile cancer, prostate cancer, chronic or acute concer, renal cell carcinoma, bladder cancer, kidney cancer, ureter CC cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC sacer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, brimary concernor new anticarcer sacer. The protein is useful as a target for acreament and pelvic carcinoma, cancer, acreament cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-627822/61.
N-PSDB; ADR86548.
    Sequence 312 AA;
                                                                        screening new anticancer agents. The present sequence represents 312 amino acid sequence of p38/JTV-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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          06-JUN-2001; 2001US-029949F; 11-JUN-2001; 2001US-029573P; 11-JUN-2001; 2001US-029573P; 12-JUN-2001; 2001US-0295573P; 12-JUN-2001; 2001US-0295573P; 12-JUN-2001; 2001US-0299585P; 15-JUN-2001; 2001US-0299585P; 15-JUN-2001; 2001US-0299390P; 19-JUN-2001; 2001US-0299390P; 19-JUN-2001; 2001US-0299390P; 19-JUN-2001; 2001US-0300883P; 19-JUN-2001; 2001US-0301530P; 28-JUN-2001; 2001US-0301530P; 28-JUN-2001; 2001US-0301530P; 28-JUN-2001; 2001US-0301550P; 13-JUL-2001; 2001US-0302951P; 13-JUL-2001; 2001US-0302951P; 13-JUL-2001; 2001US-0302951P; 13-JUL-2001; 2001US-0302951P; 13-JUL-2001; 2001US-0337477P; 14-DEC-2001; 2001US-0337477P; 14-DEC-2001; 2001US-0337477P; 14-DEC-2001; 2001US-0339656P; 12-FEB-2002; 2002US-0359658P; 22-FEB-2002; 2002US-0359034P; 22-FEB-2002; 2002US-0359034P; 22-FEB-2002; 2002US-0359964P; 12-MAR-2002; 2002US-036958P; 12-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036371346P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002US-036376P; 11-MAR-2002; 2002U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOVX polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA
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2001US-029641BP.
2001US-029657BP.
2001US-029573P.
2001US-0295573P.
2001US-0297567P.
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18-NOV-2004

(first

entry

ADR86553 standard;

protein;

229

B

84-312 amino acid sequence of p38/JTV-1 protein.

p38/JTV-1; Cytostatic;

cancer; leukemia;

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Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 226; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK,
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
Burgess CE, Lepley DM;
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     245
                                                                      185
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DB; ADC10203.
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                                                                                     HNAVTLTLIDSWVDIAMFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSV
                                                                                                                                                LVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQK 224
                                                                                                                                                                                                 ALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPEN
LQQIGGCSVTVPANVQRWMRSCENLAPF
                   LQQTGGSSGAAPTNVQRWLKSCENLAPF 312
                                                           HNAVNATLIDSWYDIAIFOLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSV
                                                                                                                              LLKCFGEQNKKÓPRODYÓLGFTLÍWKNVPKTÓMKFSIÓTMCPIEGEGNIARFLFSLFGÓK
                                                                                                                                                                                                                   TLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPEN
                                                                                                                                                                                                                                                                  QEESNLSLQALESRODDILKRLYELKAAVDGLSKWIQTPDADLDVTNIIQADEPTTLTTN
                                                                                                                                                                                                                                                                                                                                                                                                               272
                                                                                                                                                                                                                                                                                      OBTSEPSLQALESRODDILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATN
                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                         74.4%;
88.4%;
                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Score 1232; DB 7;
Pred. No. 5.1e-118
                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                184
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RESULT 7
ADR86552
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AC ADR8
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AC ADR8
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AT 18-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to an isolated p38/JTV-1 protein for use as CC medicament. The p38/JTV-1 protein or the pharmaceutical composition is CC useful as medicament for treating breast cancer, large intestinal cancer, CC lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, CC cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, CC rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, CC endometrial carcinoma, cervical cancer, wlval cancer, vaginal carcinoma, CC endometrial cancer, parathyroid cancer, small intestine cancer, endocrine CC cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue CC encer, thyroid cancer, parathyroid cancer, prostate cancer, chronic or acute CC cutanour, urethral cancer, parathyroid cancer, prostate cancer, chronic or acute CC cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC CNS lymphoma, back marrow tumour, brain stem nerve gliomas, pituitary CC cancer their combination. The protein is useful as a target for CC screening new anticancer agents. The protein sequence represents the 84-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                   18-NOV-2004
                                                         ADR86552;
                                                                                             ADR86552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 6; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1454628-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                                                                     GRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQRWLKSCENIAPF 312
                                                                                                                                                                                                                                                                                                                                             EHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQT
                                                                                                                                                                                                                                                                                                                                                                             ERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQMKFSVQT
                                                                                                                                                                                         GKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQRWMRSCENLAPF
                                                                                                                                                                                                                                                                     MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                                                                       MCPIEGEGNIARFLESLEGOKHNAVTLTLIDSWVDIAMEQLREGSSKEKAAVERSMNSAL
                                                                                                                                                                                                                                                                                                                                                                                                                           DADLDVINIIQADEPTTLTINALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                   (first
                                                                                             protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.6%; Score 1069; DB 8; 88.2%; Pred. No. 2.6e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 229;
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RESULT 8
ABP01502
ID ABP0
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AC ABP0
XX
DT 24-J
XX

ABP01502;

ABP01502 standard;

protein;

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120 60 8

24-JUN-2002

(first entry)

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                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
                                                                                                                                                                                                                                                                                                            Sequence 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAR-2003; 2003KR-00013058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2003; 2003EP-00020344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p38/JTV-1; Cytostatic; cancer; leukemia; anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-161 amino acid sequence of p38/JTV-1 protein.
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                                                                                                                                                                                                                                                 Local Similarity
121
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                                  121
                                                                                                                                                                                                                               143;
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                                                                                                             61
                                                                                                                                                    _
                                                                                                                                                                                        1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                    DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNV 161
                                                                                                   DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV 161
                                                                        DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                    MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
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                                                                                                                                                                                                                                                 Score 735; DB 8;
Pred. No. 4.4e-67;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders, haemorrhage, osteoarthritis, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the protein are also resent the prot
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide syndrome associated with ORFX-associated disorder. ORFX polymucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2986; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-106308/14.
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29-AUG-2000;
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                                                                                                                                                                                                                                           Local Similarity
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                                                   DGLSKMIHTPDADLDVINILQADEPTTLATNTLDLNSVLGKDYGALKDIVI 124
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DGLSKMIHTPDADLDVTNILQADEPTTLTTNALDLNSVLGKDYGALKDIVI
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2000US-0228716P.
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                                                                                                                                                                                  Score 248; DB Pred. No. 1.3e 0; Mismatches
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1.3e-17;
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Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 14196; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic
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                           ISSPTMYVPIYGEVNIIRYLGRVGPAEYRYEGSPLCNEIDLVLDICYQLLRCNTHKTQVA
                                                       KFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTL---IDSWVDIAMFQLREGSSKEKAA
                                                                                                              RYRVLSTVHTHSSVKNV-----PENLVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQM
                                                                                                                                             AGLGVCG--KTFOHTTAFONG------GLKEVPLODVVINGHPNFIPYALLALKNAWRN
                                                                                                                                                                         ADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCE 144
                                                                                                                                                                                                      RTGRNAATCALDLDSLGRQIQRLLKDDTASVAARQEKVLKQLEELKAQLGQIR-----
                                                                                                                                                                                                                                                               MYELKTL---LPQFDIKLPTCMYPLKNVSLAADSLASGSSTSASTSASTSSCKLEANRID
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2000US-00614150.
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Pred. No. 4.8e-13;
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84 5.1 443 4 US-09-949-016-10598 5.1 646 4 US-09-248-798-18678 84 5.1 1057 4 US-09-428-156B-2 83.5 5.0 360 4 US-09-949-016-10589 83.5 5.0 475 4 US-09-949-038-8208 83.5 5.0 515 4 US-09-9489-0398-8208 83.5 5.0 515 4 US-09-9489-0398-8208 83.5 5.0 519 4 US-09-543-81A-6505 83.5 5.0 789 3 US-09-5285-84 83.5 5.0 789 4 US-09-589-477-84 83.5 5.0 789 4 US-09-589-478-84 83.5 5.0 789 4 US-09-580-884 83.5 5.0 789 4 US-09-580-878-84 83.5 5.0 789 4 US-09-580-1016-1016-1016-1016-1016-1016-1016-10	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	
.1 443 4 US-09-949-016-10598 .1 646 4 US-09-248-796A-1867 .1 1057 4 US-09-248-156B-2 .0 360 4 US-09-949-016-10589 .0 475 4 US-09-389-352-5379 .0 519 4 US-09-543-681A-6505 .0 519 4 US-09-543-681A-6505 .0 789 3 US-09-002-285A-84 .0 789 4 US-09-589-477-88 .0 789 4 US-09-589-477-88 .0 789 4 US-09-581A-6879 .0 434 3 US-09-120-601-6 .0 434 3 US-09-120-601-6 .0 448 3 US-09-120-601-6 .0 559 4 US-09-821-016-1 .0 559 4 US-09-821-016-1 .0 559 4 US-09-821-016-1 .0 559 4 US-09-821-057-8	83	83	83	83	83	83	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	84	84	84	
4 US-09-949-016-10598 4 US-09-248-796A-1867 4 US-09-248-156B-2 4 US-09-949-016-10589 4 US-09-949-035-82-5379 4 US-09-489-039A-8208 4 US-09-543-681A-6505 4 US-09-589-477-84 4 US-09-589-477-84 4 US-09-589-477-84 4 US-09-589-47-84 3 US-09-012-072-4 3 US-09-012-072-4 3 US-09-120-601-4 3 US-09-120-601-6 4 US-10-961-1016-1 4 US-10-961-1016-1 4 US-10-961-797-1 3 US-09-1266-787-8	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0		5.1	5.1	5.1	
0598 1867 0589 0589 0589 0589 05820 6820 6820 684	767	559	559	448	434	434	959	789	789	789	519	515	475	360	1057	646	443	
0598 1867 0589 0589 0589 0589 05820 6820 6820 684	w	4	4	w	ω	w	4.	4	4	w	4.	4	4	4	4	4	4	
	US-08-836-567-8	US-10-266-787-1	US-09-821-016-1		US-09-120-601-4	US-09-012-072-4	US-09-543-681A-6879	US-10-099-285A-84	US-09-589-477-84	US-09-002-285-84	US-09-543-681A-6505	US-09-489-039A-8208	US-09-328-352-5379	US-09-949-016-10589	US-09-428-156B-2	US-09-248-796A-18678	US-09-949-016-10598	
	8, Appli	1, Appli	1, Appli	6, Appli	4, Appli	4, Appli	6879, Ap	84, Appl	84, Appl	84, Appl	6505, Ap	8208, Ap	5379, Ap	10589, A	2, Appli	18678, A	10598, A	

US-09-949-016-11312

ALIGNMENTS

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Sequence 11312, Application US/09949016

PALENT NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-31

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11312
LENGTH: 341
TYPE: PRT
ORGANISM: Human
US-09-949-016-11312
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Best Local S
Matches 279
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Local Similarity 87.2%;
les 279; Conservative 10
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301
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                                                                                                                                                                             DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                      DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
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RWLKSCENLAPFSTALQLLK 320
                                                      MFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ
                                                                                                                          YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA
                                                                                                         YOLGFTLIWKNVPKTOMKFSIOTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                 I FOLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
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; TELEFAX: 202-508-9299;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-518-862C-2
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US-08-518-862C-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Micolaides, Nicholas C.
APPLICANT: Nicolaides, Nicholas C.
APPLICANT: Nicolaides, Nicholas C.
APPLICANT: NICOLAIDES PMS2 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08518862C Patent No. 5843757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: KAGAI, SATAL A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,862C
FILING DATE: 24-AUG-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Banner & Witcoff, Ltd. STREET: 1001 G Street, N.W. CITY: Brington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                        RWLKSCENLAPF 312
                                                                                     MFQLREGSSKEKAAVFRSMVSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ 300
RWMRSCENLAPF 312
                                                                IPQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ 300
                                                                                                                                            YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
                                                                                                                                                                    YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA 240
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RWMRSCENLAPFNTALKLLK 341
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APPLICANT: LAI, PREETI
APPLICANT: LAI, PREETI
FILE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
CURRENT APPLICATION NUMBER: US/09/443,184A
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
SEQ ID NO 48
LENGTH: 1512
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAMEKEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1
US-09-443-184-48
                                                                                           APPLICANT: Falco, S. Carl
APPLICANT: Fancou, Layo O.
APPLICANT: Fancou, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-trna Synthetase
FILE REFERENCE: BB-1193
CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60/093,530
EARLIER FILING DATE: July 21, 1998
INUMBER OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
ISSOFTWARE: Microsoft Office 97
;
ORGANISM: Homo sapiens
US-09-357-251-37
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                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09357251 Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.4%; Score 106; DB 3; Length 1512; Best Local Similarity 21.8%; Pred. No. 0.096; Matches 44; Conservative 33; Mismatches 69; Indels 5
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                                                  LENGTH: 1440
TYPE: PRT
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APPLICANT: Zweiger, Gary
APPLICANT: Kaser, Matthew R.
APPLICANT: Panzer, Scott
APPLICANT: Seilhammer, Jeffrey J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yue, Henry
APPLICANT: Baughn, Mariah
APPLICANT: Azimzai, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 KKAPVHVKRWFGFLEAQQAFQS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 GFTLIWKNVPKTOMKFSVQTMCPIEGEGNIARFL----FSLFGQKHNAVTLTLIDSWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 INANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHEYQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LTVNSGDPPLGALL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFSATKL--SSCDSFTSTINELNHCLSLRTYLVGNSLSLADLCVWATLKGNAAWQEQLKQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VSENVIFTDV------NSILRYLARVATTAGLYGS--NLMEHTEIDHWL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAPTNVQRWLKSCENLAPFST 314
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Mon Feb 28 10:03:52 2005
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Regult
No.
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Maximum DB
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Maximum Match 10
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
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        1436
1069
105.5
105.5
103.5
99.5
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96.5
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1: /cgm2 6/ptcdata/1/pubpaa/PCT NEW PUB.pep:*

2: /cgm2 6/ptcdata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgm2 6/ptcdata/1/pubpaa/USO6 NEW PUB.pep:*

4: /cgm2 6/ptcdata/1/pubpaa/USO6 NEW PUB.pep:*

5: /cgm2 6/ptcdata/1/pubpaa/USO7 NEW PUB.pep:*

6: /cgm2 6/ptcdata/1/pubpaa/USO8 NEW PUB.pep:*

7: /cgm2 6/ptcdata/1/pubpaa/USO8 NEW PUB.pep:*

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10: /cgm2 6/ptcdata/1/pubpaa/USO9 PUBCOMB.pep:*

11: /cgm2 6/ptcdata/1/pubpaa/USO9 PUBCOMB.pep:*

12: /cgm2 6/ptcdata/1/pubpaa/USO9 PUBCOMB.pep:*

13: /cgm2 6/ptcdata/1/pubpaa/USO9 PUBCOMB.pep:*

14: /cgm2 6/ptcdata/1/pubpaa/USO9 PUBCOMB.pep:*

15: /cgm2 6/ptcdata/1/pubpaa/USO9 PUBCOMB.pep:*

16: /cgm2 6/ptcdata/1/pubpaa/USO0 PUBCOMB.pep:*

16: /cgm2 6/ptcdata/1/pubpaa/USO0 NEW PUB.pep:*

16: /cgm2 6/ptcdata/1/pubpaa/USO0 NEW PUB.pep:*

17: /cgm2 6/ptcdata/1/pubpaa/USO0 NEW PUB.pep:*

18: /cgm2 6/ptcdata/1/pubpaa/USO0 NEW PUB.pep:*

19: /cgm2 6/ptcdata/1/pubpaa/USO0 NEW PUB.pep:*

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length: 2000000000
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Listing first 45 summaries
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                      16 US-10-463-676-4
16 US-10-463-676-5
16 US-10-463-676-5
16 US-10-437-963-126132
15 US-10-424-599-260388
16 US-10-437-963-15387
18 US-10-282-122A-44369
19 US-09-815-242-5841
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Sequence 4, Appli
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Sequence 5, Appli
Sequence 126132,
Sequence 6336, Ap
Sequence 260388,
Sequence 153870, A
Sequence 44389, A
Sequence 5841, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 123304,
Sequence 123304,
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ALIGNMENTS

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PRIOR FILING DATE: 2003-03-03
NUMBER OF SEO ID NOS: 17
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 312
TYPE: PRT
                                                                                                                                          Query Match
Best Local Similarity 87.9
Matches 273; Conservative
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Publication No. US20040175375A1
GENERAL INFORMATION:
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APPLICANT: Park, Bum-Joon
TITLE OP INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
TITLE OP INVENTION: for Screening Pharmaceutical Composition for Treating
FILE REFERENCE: 012679-091
CURRENT PPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
FEATURE:
RAME/KEY: PEPTIDE
LOCATION: (1)...(312)
OTHER INFORMATION: 1-312 amino acid sequence
                      13
DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
                                                                                     MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                               MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
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87.5%; Pred. No. 2.60
tive 14; Mismatches
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RESULT 3
US-10-463-676-5
; Sequence 5, Application US/10463676
; Publication No. US20040175375A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Sunghoon
; APPLICANT: Park, Bum-Joon
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US-10-463-676-6
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CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 229
TYPE: PRT
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Publication No. US20040175375A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: PEPTIDE
LOCATION: (1)...(229)
OTHER INFORMATION: 84-312 amino acid sequence p38/JTV-1
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ilarity 88.2%;
Conservative 1;
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Pred. No. 4e-100;
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_28709C.1.pep
US-10-437-963-126132
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TYPE: PRT

CORGANISM: Homo sapiens

FEATURE:

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)...(161)

OTHER INFORMATION: 1-161 amino acid sequence of p38/JTV-1

US-10-463-676-5
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SEQ ID NO 126132
LENGTH: 925
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APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaruk, Brad
APPLICANT: Barbaruk, Brad
APPLICANT: Li, ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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83 PDADLDVTNILQAD--EPTTLATNTLDLNSVLGKDYGA----
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ative 46; Mismatches
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Pred. No. 2.5e-66;
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86	87	87.5	87.5	88	88	88	88.5	88.5	89	89	89	89	89	89.5	89.5
5.2	5.3	5.3	σ. ω	5.3	5.3	5.3	5.3	5.3	5.4	5.4	5.4	5.4	5.4	5.4	5.4
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T45158	T15763	H82302	B70597	T38906	T42531	T24728	H84206	AB3542	A33812	G02157	T31669	AE2443	S74356	T14165	S18644
pre-mRNA splicing	hypothetical prote	ATP-dependent heli	hypothetical prote	acetyl-CoA carboxy	acetyl-CoA carboxy	hypothetical prote	acetyl-CoA synthet	gtp-binding protei	interphotoreceptor	kinesin-like spind	neural zinc finger	penicillin-binding	glutathione S-tran	peptide synthetase	multifunctional am

ALIGNMENTS

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-728 <DAV>
A;Residues: 1-728 <DAV>
A;Cross-references: UNIPROT:065253; EMBL:AF058914; NID:g3047074; PID:g3047084; GSPDB:GNU
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                     probable glutamate-tRNA ligase (EC 6.1.1.17) F21B10.12 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T01200 C;Accession: T01200 R;Davidson, S.; Rohlfing, T.; David, M.; O'Brian, D. submitted to the EMBL Data Library, April 1998 A;Description: The sequence of A. thaliana F21E10.
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
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T52043
probable glutamate-tRNA ligase (EC 6.1.1.17) [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52043
R;Day, I.S.; Golovkin, M.; Reddy, A.S.
Blochim. Biophys. Acta 1399, 219-24, 1998
A;Title: Cloning of the cDNA for glutamyl-tRNA synthetase from Arabidopsis thal A;Reference number: Z24836; MUID:9765600; PMID:9765600
A;Accession: T52043
                                                                                                                                                                 A; Description: The sequence A; Reference number: Z14258 A; Accession: T01200
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C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology
C;Keywords: ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 PASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHEYQLGFTL 187
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A;Mat position: 5
A;Introns: 25/3; 215/2; 266/3; 540/3; 585/3; 786/1, C;Superfamily: insulin-degrading enzyme (IDE) C;Keywords: hydrolase; metalloproteinase; zinc F;70,74/Binding site: zinc (His) #status predicted F;73/Active site: Glu #status predicted
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A;Cross-references: UNIPROT:Q17592; EMBL:U55372; PIDN:AAA98001.1; GSPDB:GN00023; CESP:CqA;Experimental source: strain Bristol N2; clone C02G6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable zinc proteinase (EC 3.4.24.-) C02G6.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2 C;Accession: T30089 R;Bentley, D.; Kemp, K.; Scheet, P. submitted to the EMBL Data Library, April 1996 A;Description: The sequence of C. elegans cosmid C02G6.
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T30089
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A;Accession: T30089
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Map position: 5
A;Map position: 5
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: yeast glutamate-trNA ligase; glutamine-trNA ligase homology C;Keywords: aminoacyl-trNA synthetase; ligase; protein biosynthesis F;223-499/Domain: glutamine-trNA ligase homology <EGL>
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Best Local Similarity
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                                                                                          392
            446
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                                                                                                                                                                                                                                                                           10 HGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQDDILKRLYE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
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                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 PASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHEYQLGFTL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
KMKKYENALKTSHHALHLPEKN--EYIATNFGQKPRESVKNEHPKLISDDGWSRVWFKQD
                                     -----VLSTVH--THSSVKNVPENLVKCFGEQARKQSRHEYQL----
                                                                           LTKYEPERIKELLSTLTPSN-----MLVRVVSQKFKEQEGNTNEPVYGTEMKVTDISPE
                                                                                                                                                         IGMLKSF--GPQQWIHDELADLSDVKFRFKDKEQPMKMAINIAASLQYIPIEHILSSRYL 391
                                                                                                                                                                                               ---LKAAVDGLSKMIHTPDADL-DVT-NILQADEPTTLATNT-----LDLNSVLGKDY- 116
                                                                                                                                                                                                                                       HKGPGSLLVELKRLGW-VNSLKSDSNTIAAGFGILNVTMDLSTGGLEN-VDEIIQLMLNY 333
                                                                                                                     -----GALKDIVINANPASPPLSLLVLHRLLCERYR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLT-----LJDSWVD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YASV-FSSGSEFENAC--GRVDKYLESSTFLVGHSLSIADVAIWSALAGTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAMFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLMSVLQQTGGSSGAAPTN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PESPPLSVIVALSISASPV----TIDSSAAATTVPSFVF----SDGRKLN-----GATV 55
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
                                                                                                                                                                                                                                                                                                                       6.3%; Score 104; DB 20.1%; Pred. No. 2.1; tive 67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 112; DB; 26.6%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                         Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GRSAKKLPDFYG--NNAFDSSQVSILCINMKIDEWVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   786/1;
                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                             Length 980;
                                                                                                                                                                                                                                                                                                                     Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                       -GFTLIW----
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89797
R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L;
ma, A, Mizutani-Ui, Y; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu,
C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lancet 357, 125-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: geh
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q99WQ6;
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-691 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       623 ----RTLTNHAFSQPYLLTQHYNQLLIVDKV-WSKEQLLAVCDSVTLENVQGFAR--EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 DEYNWEKQETKFALTTPIVSQNPRISLISSLWLWCFCDILSEETYNAALAGLGCQFELSP
                                                                                                                                                                                                                                                                                                                                                                                            1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDA------GHVQETSEPSL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 --KNVPKTQMKFSVQT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                  KEKAAVFRSMNSALGRSPWLVG 271
                                                                 AAHAAKYGHERYGKTYKGIMPNWEPGKKVHLVGHSMGGQTIRLMEEF---
                                                                                                                                       GDNAPALYPNYWGGNKFKVIEELRKQGYNVHQASVSAFGSNYDRAVELYYYIKGGRVDYG
                                                                                                                                                                        PENLVKCFG------EQARKQSRHEYQLGFTLIWKNVFK-TQMKFSVQTMCFIEG
                                                                                                                                                                                                                                                ATNTLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNV 161
                                                                                                                                                                                                                                                                                     QIIDAKQDDTV-RQSEQKPQVGDLSKHIDGQNSPEKPTDKNTDNKQLIKDALQA--PKTR
                                                                                                                                                                                                                                                                                                                        QALESRODDILKRLYELKAAVDGLSKMI---HTPDADLD----VTNILQADEPTTL
                                                                                                                                                                                                                                                                                                                                                           IPAQKVLPNHDKAAPTSTTPPS-----NDKTAPKSTKAQDATTDKHPNQQDTHQPAH
                                                                                                        EGNIARFLFSLFGQKHNAV------
KEEIAYHKAHGGEI--SPLFTG
                                                                                                                                                                                                                     STINAAAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus triacylglycerol lipase
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%; Score 99; DB 2; Length 691
20.2%; Pred. No. 3.4;
ative 53; Mismatches 110; Indels
                                                                                                                                                                                                                     AKKVRPLKANOVOP
450
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                                                                                                                                                                                                               ----LNKYPV---VFVHGFLGLV
                                                                                                    TLTLIDSWVDIAMFQLREGSS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                 LRNG-N 430
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probable glutathione S-transferase VCA0584 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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5 homo sapien
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6 xenopus tro
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8 drosophila
9 drosophila
9 drosophila
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2 arabidopsis
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7 romo sapien
7 pseudomonas
7 homo sapien
9 gloeobacter
7 caenorhabdi
0 corynebacter
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0 corynebacter
7 caenorhabdi
0 corynebacter
7 caenorhabdi
0 corynebacter
8 pseudomonas
9 photorhabdi
0 trachydanio
4 brachydanio
7 vibrio vuln
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98	98	98.5	98.5	98.5	99	99	99	99	99	99	99.5	100.5	100.5	
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690	240	1597	377	222	691	691	691	690	690	559	922	885	555	
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P10335 stap		Q8v9a2 cruc	026161 meth			q99wq6 stap		Q6gcf1 stap	Q8nyc2 stap			Q8k2j4 mus		
staphylococ	mus musculu	crucifer to	methanobact	rio chol	staphylococ	staphylococ	staphylococ	staphylococ	staphylococ	pseudomonas	brachydanio	mus musculu	vibrio vuln	

ALIGNMENTS

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Q8R2Y6
                                                                                                                                                                                                                                                   RX STRAIN-CZECH II; TISSUE-Mammary tumor;
RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shammen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rodristein M.J., Wagner P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., McCEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Lones S.J., Marra M.A., in Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
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Best Local S
Matches 320
                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CZECH II; TISSUE-Mammary
Strausberg R;
Submitted (APR-2002) to the EMBI
EMBL; BC026958; AAH26958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CZECH II; TISSUE=Mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-JUN-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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21,
26,
                  EMBL/GenBank/DDBJ databases
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Last annotation update)
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Best Local S
Matches 319
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16-OCT-2001 (Rel. 40, Createu,
16-OCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Multisynthetase complex auxiliary component p38.
Cricetulus griseus (Chinese hamster).
Eukaryota; Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metzaca; Chordata; Sciurognathi; Muridae; Cricetinae;
                                                      This SWI
between
the Euro
                                                                                                                                                                                                                  MEDITINE-99096915; PubMed=9878398; DOI=10.1006/jmbi.1998.2316; Ouevillon S., Robinson J.-C., Berthonneau E., Siatecka M., Mirande M., Macromolecular assemblage of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characterization a core protein."; J. Mol. Biol. 285:183-195(1999).

-I- FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ovary;
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InterPro; IPR004046; GST_Clike
InterPro; IPR001987; GST_C_like
Pfam; PP00043; GST_C; 1.
SEQUENCE 320 AA; 35423 MW;
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                   Structure.

SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxil proteins, p18, p48 and p43.

SIMILARITY: Contains 1 GST-like domain.
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Pred. No. 4
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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HUMAN
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                                                                                                                                                                                    Genomics
[2]
                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-96115582; PubMed=8666379;

Nicolaides N.C., Kinzler K.W., Vogelstein

"Analysis of the 5' region of PMS2 reveals

and a novel overlapping gene.";
                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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29:329-334(1995).
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Primates;
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No. 1.6e-121;
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121

DIVINANPASPPLSLLVLHRLLCERYRYLSTVHTHSSVKAVPENLVKCFGEQARKQSRHE

DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD

120 120 S

MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD

Query Match Best Local S Matches 279

Similarity

35349 MW; 88.5**%**; 87.2**%**;

F253726B63C12BAB CRC64;

Conservative

16;

Score 1464; DB 1; Pred. No. 1.6e-112; 6; Mismatches 25;

Length

320;

Indels

0

Gaps

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Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., rain v......

Lee S.W., Han J.M., Lee H.-W., Kim S.;

"Downregulation of FUSE-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation.";

Nat. Genet. 34:330-336(2003).

-I- FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular mediates ubiquitination of FUBP1 and its degradation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang C.
Liu M.,
                                                                                  H-InvDB; HIX0006460;
MIM; 600859; -.
                                                                                                                     EMBL; U24169; AAC50391.1; ALT_FRAME
EMBL; BC002853; AAH02853.1; -.
EMBL; BC00156; AAH10156.1; -.
EMBL; AF116615; AAF71039.1; -.
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahey J., Helton E., Ketteman M., Madan A., Rodriques S., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rotterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full
                                                                                                                                                                                                           entities requires a license agreement (Su or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.
                Protein
                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22716800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 197-320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Villalon D.K., Muzny D.M.,
                                                                interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH FUBP1
                                                                                                                                                                                                                                                                                                                                                                 structure. Mediates ubiquitination of FUBP1 and its degradati the proteasome.

SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxil proteins, pls, p48 and p43. Binds FUBP1.

SIMILARITY: Contains 1 GST-like domain.

SIMILARITY: Ref. 1 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                frameshift in position 312.
                               Pro; IPR010987; GST_C_like
Pro; IPR004046; GST_Cterm.
PF00043; GST_C; 1.
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biosynthesis
E 320 AA;
                                                                                                                                                                                                                                             non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12819782; DOI=10.1038/ng1182;
-J., Kang Y.-S., Kim H.J., Park J.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sci. U.S.A.
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                                                                                                                                                                                                                      oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.,
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Bouffard G.G.,
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gues S., San
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RX MEDLLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausmer R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA RATSywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                         Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013630, AAH13630.1; -.
InterPro; IPR004046; GST Cterm.
IntexPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
Pfam; PF00043; GST_C; 1.
SEQUENCE 320 AA; 35335 MW; 19F14BF758612E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                       88.2%; Score 1460; DB 2;
86.9%; Pred. No. 3.4e-112;
tive 16; Mismatches 26;
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Last sequence update)
Last annotation updat
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RM MEDININE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Feeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Ra Hithing M., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ra Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willing M., Madan A., Young A.C., Shevchenko Y., Butfard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

VA Jones S.J., Marva M.A.;
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                                                                                                     InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
Pfam; PF00043; GST_C; 1.
SEQUENCE 280 AA; 31097 MW; E5BE81498983FD2E CRC64;
                                                                                                                                                                                EMBL; BC024480; AAH24480.1; MGD; MGI:2385237; Jtv1.
                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Mammary tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8R3V2;
Q8R3V2;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                       "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Jtv1;
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                                       276;
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                                                            Similarity
QETSEPSLQALESRQDDILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATN 104
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                                         Conservative
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                                                    85.3%; Score 1412;
100.0%; Pred. No. 2.
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Sciurognathi; Muridae; Murinae; Mus
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[2]
SEQUENCE FROM.
SEQUENCE FROM.
TISSUE=Embryo;
A Klein S., Gerhard D.S.;
AL Submitted (JUN-2004) to the EMBL/Genative Embry E0704561; AAH74561.1; -.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR010987; GST_C_like.
Therefore JIR010987; GST_C; 1.
Therefore 311 AA; 34480 MW; D9'
FOR THE BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN BROWN B
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Woorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

A Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;
                                   Query Match
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Matches 216
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; 
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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TISSUE-Embryo;
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                                                                       Local Similarity
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Last annotation updat
                                                                       Score 1153.5; DB 2; Length 311; Pred. No. 6.8e-87;
                                                                                                                                                                                       D98F27F73C466154 CRC64;
                                       Mismatches
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A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

K Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Diatchenko J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marya M.A.,

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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                               Variable M.A.;

Jones S.J., Marra M.A.;

"Generation and initial analysis of and mouse cDNA sequences.";

proc. Natl. Acad. Sci. U.S.A. 99:16
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                           Klein S.L., St
Richardson P.;
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                                                                               "Genetic and genomic tools for initiative.";
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                                                                   initiative.
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McZewan P.J., McKernan K.J., Make J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA RA Haiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Radininski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Submitted (JUN-2004) to the EMBL/G
EMBL, BCO72178, AAH72178.1; -.
InterPro, IPR004046; GST_Cterm.
InterPro, IPR010987; GST_C like.
Pfam, PP00043, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, GST_C, 
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Amphibia; Batrachia; Anura;
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a; Batrachia; Anura; Mesobatrachia; Pipoidea;
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Q7T3C0;
Q1-OCT-2003
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01-MAR-2004
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Submitted (JAN-2003) to the EMBL/(
EWBL; BC043832, AAA443832.1; -.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C_1 I._
Pfam; PF00043; GST_C, 1._
SEQUENCE 311 AA, 34647 MW; 2F(
                                                                    Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; 1
Cyprinidae; Danio.
                                                                                                       Zgc:63976.
ORFNames=zgc:63976;
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_Strausberg R.L., Wagner
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Teleostei;
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annotation update)
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r L., Pontius J., Clifton
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ta; Vertebrata; Eu
ei; Ostariophysi;
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SEQUENCE FROM N.A.

TISSUB-Kidney;

TISSUB-Kidney;

MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler (
Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.)

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NCBI_TaxID=7955;

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                                                                        AgCP5808 (Fragment).
Name-agCG50514; ORFNames=ENSANGG00000011827;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Nematocera; Culic
  SEQUENCE
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Submitted (JUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKQSRHEYQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFG-QKHNAVTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYGALKDIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFG-EQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTS---PATDAGHVQETSEPSLQALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SAPANVQRWLKSCQNLGYFSCVDPLLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDGWVDTALFQLAEGGSKERAAVLRALNAALGRSPWLLGQEFSLADIVSACCVLQTGQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDSWVDIAMFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIGALRDIVINANPAQPPLSLLVLHALLCQRFQVLSSVHVHSSVSTVPAPLLSCLGPRHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPMYQVKPV--SPADITVDLPTCMYKLPNVHAQGASLGEHALQNGEV----DPTVKALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34852 MW; BA8F6B951208244A CRC64;
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Last
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Pred. No. 4.1
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                                                                           ecta; Pterygota;
Culicoidea; Ano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases.
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RESULT 12
Q7KUM5
ID Q7KUM5
AC Q7KUM
AC Q7KUM
DT 05-JU
DT 05-JU
DT 05-JU
DT 05-JU
DT 05-Webst
GN ORFMW
OS Drose
OC Neoply
OC Ephyy
OC NEOPLY
RP SEQUI
RP SEQUI
RP SEQUI
RA Adamu
RA Adamu
RA Adamu
RA Adamu
RA Adamu
RA Adamu
RA Adamu
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RA Burt:
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RX MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185; An Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gacayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Stutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Champe M., Pfeiffer B.D., RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., RA Baril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Baslew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7KUM5;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=CG12304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG12304-PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7KUM5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THSSVKNVPE-----NLVKCFGEQARKQSRHEYQLGFTLIWKNV-PKTQMKFSVQTMCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SALGRSPWLVGNELTVADVVLWSVLQQ 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLKSKAQLKAEPINLT------CLQDFVVNASPEYVPYSLLALKNLWKDRLNLQVECF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LATNTLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCERYRVLSTVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLLQKAENDELRMLAERQQRVLQQLAELK-----KEIMAMRTELKLNANAPPAVQPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYRLKPVM--NQDVVCELPTCMYTLKPVCAYSHDPKAFSADSATGLAAAGPVDPMSIEID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THSTVPKLSEEALAFQNAVTASGTAAANLPR----IKVTLIWKNVGAYTEMITSPTSYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. : (TrEMBLrel. : )
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27,
27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 247; DB 2; Le
Pred. No. 6.1e-12;
9; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247; DB 2;
No. 6.1e-1;
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RA

Ablali M., Kalush F., Karpen G.H., Wei M.H., Ibegwam C.,

RA

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA

RA

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA

Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA

RA

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA

RA

Ralisson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA

Ralizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA

Reinert K., Remington K., Sunders R.D., Scheeler F., Shen H.,

RA

Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA

Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA

Williams S.M., Moodaget, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA

Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu S., Smith H.O.,

RA

Zience 287:2185-2195(2000).
       Query Match
Best Local S
Matches 86
                                                      Flybase;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ
EMBL; AE003530; AAS64998.1; -
InterPro; IPR004046; GST Cterm.
InterPro; IPR010967; GST C_like.
Pfam; PF00043; GST_C; 1.
Pfam; PF00043; GST_C; 1.
SEQUENCE 301 AA; 33241 MW; 35224E17FE03F3;
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin."
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01-MAR-2004
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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Bukaryota; Metazoa; Arthropoda; Harapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;
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ORFNames=CG12304;
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Best Local S
Matches 86
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Q9VUR3;
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
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Stapleton M., Carlson J., Chavez C., Frise E., George R.
Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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             RA Abril J.F., Abgayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Debther A., Deng Z., Mays A.D., Dew I. Dietz S.M., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Calce R., Chardra I., RA Doddon K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Doddon K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glann H., Houck J., RA Harris N.L., Harvey D.A., Herman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D.A., Herman T.J., Hernandez J.R., Houck J., RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mohrefi A., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Reinert K., Wassarman D.A., Weinsteon M., Skupski M.P., Smith T., RA Palazzolo M., Holland S.M., Wassarman D.A., Weinsteok G.M., Weissenbach J., RA Yellon K.A., Modasy C., Stapleton M., Skupski M.P., Smith T., RA Wang Z.-Y., Wassarman D.A., Weinsteok G.M., Weissenbach J., RA Yellon K.A., Zhong F.N., Rab, R., Shon M., Zhang G., Zhao Q., Zheng L., Rha Yellon K.A., Zhong F.N., Rab, R., Shu M., Smith H.O., Ra Zheng X., Zhang G., Zhao Q., Zheng L., The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                          MEDLINE=22420069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Milthourn G.H., Prochnik S.E.,
Hradecky P., Huang Y., Kaminker J.S., Milthourn G.H., Berchnik S.E.,
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                                                                                                                                                                                                                                                 "Annotation of the Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                            Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
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FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure (By similarity).

SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43 (By similarity).

SIMILARITY: Contains 1 GST-like domain.
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FlyBase; FBgn0036515; CG12304.
InterPro; IPR010987; GST C like.
InterPro; IPR0104046; GST_Cterm.
Pfam; PF00043; GST C; 1.
Protein blosynthesis.
DOMAIN 280 327 GST-1:
SEQUENCE 334 AA; 36933 MW; B681
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                                                                                                                                               216
                                                                 276 MVRLLDKRLQKQQYFGGSQMSVADVGVYSSL 306
                                                                                            255 VFRSMNSALGRSPWLVGNELTVADVVLWSVL 285
                                                                                                                                                            198 KFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTL---IDSWVDIAMFQLREGSSKEKAA 254
                                                                                                                                                                                                             162 LYTIDVKTFTHSTMADIGPAAREFEANLAKVPVNPALP-----KISVTLIWKNCEHTEM
                                                                                                                                                                                                                                           145 RYRVLSTVHTHSSVKNV-----PENLVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQM 197
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                                                                                                                                                                                                                                                                                                                 ADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCE 144
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36933 MW; B68FD70AE621990F CRC64;
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4: geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Aar10682	Ads21772	Abg18331	Abg17694	Aae25162	Abb91239	Abb54068	Ads20980	Aar98811	Adp23041	Adp54124	Adn03674	Abm83057	Abm83058	Adn88618	Adn88619	Adn88594	Adn88621	Adn88620	20000000
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ALIGNMENTS

RESULT 1 ADE58613 ID ADE5 ADE58613; ADE58613 standard; protein; 320 B

Human Protein Q13155, SEQ ID NO 4489.

29-JAN-2004

(first entry)

Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Homo sapiens.

WO2003016475-A2

27-FEB-2003.

14-AUG-2002; 2002WO-US025765

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

GEN HOSPITAL CORP. BAYER AG.

(GEHO) (FARB)

Woolf C, D'urso D, Befort ۳ Costigan 3

WPI; 2003-268312/26. GENBANK; Q13155.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal

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RESULT 2
ABM80843
ID ABM8
XX ABM8
XX ABM8
XX ABM8
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XX TIMC
XX TUMC
XX TUMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                               WO2004030615-A2
                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                       cervical cancer; melanoma; chromosome identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour-associated antigenic target
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                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                       leukaemia;
chromosome
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Pred. No. 7.5e
L6; Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; SEQ ID NO 2179; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer or tumor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                        DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHE
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RWMRSCENLAPFNTALKLLK 320
                                    RWLKSCENLAPFSTALQLLK
                                                                                                                 MFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ
                                                                                                                                                                                        YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA
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                                                                             I FQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
                                                                                                                                                                                                                                                                                                                           DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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Pred. No. 7.5e
16; Mismatches
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JTV1; hPMS2; probe; detection; chromosome 7; deletion; mismatch repair gene; hereditary non-polyposis colorectal cancer; homologous recombination.
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                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      to guide homologous recombination at the PMS2 locus
                                                                                                                                                                                                                                        DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTIJDLNSVLGKDYGALK
                                                                                                                                                                                                                         DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                                                                                                                                                               MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQI:TSEPSLQALESRQD
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                          RWLKSCENLAPF 312
                                                     | IPQLKEGSSKEKAAVFRSMISALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ
                                                                                 MFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ
                                                                                                                            YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA 240
                                                                                                                                                                 DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
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                                                                                                            YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA
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                                                                                                                                                                                                                                                                                                                                                  86.8%; Score 1436; DB 2;
87.5%; Pred. No. 5.6e-139;
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DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD

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                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to an isolated p38/JTV-1 protein for use as CC medicament. The p38/JTV-1 protein or the pharmaceutical composition is CC useful as medicament for treating breast cancer, large intestinal cancer, cC lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood CC cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, CC cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, blood CC cancer, anal cancer, colon cancer, fallopian tube carcinoma, CC endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, CC Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine CC cancer, thyroid cancer, parathyroid cancer, adrenal cancer, endocrine CC cancer, urbral cancer, parathyroid cancer, xidrenal cancer, endocrine CC cancer, renal cancer, parathyroid cancer, xidrenal cancer, ureter CC leukemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter CC cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC cancer, thair combination. The protein is useful as a target for CC screening new anticancer agents. The present sequence represents the 1-

CC 312 amino acid sequence of p38/JTV-1 protein.
                                                                                                                                                                                                                                                         Matches 273;
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated p38/JTV-1 protein, useful as medicament for treating e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck and cutaneous or intraocular melanoma, as well as for screening n_{\rm c}
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR86551 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-2003; 2003KR-00013058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-SEP-2003; 2003EP-00020344
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                                                                                                                                                                                                                                                                                              Similarity
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MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4; 47pp; English.
                                                                                                                                   MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry
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                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                            Score 1436; DB 8;
Pred. No. 5.6e-139;
4; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                      Length 312;
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04-UNI-2001; 2001US-02950/P

06-UUN-2001; 2001US-029561BP

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07-UNI-2001; 2001US-029575P

11-UNI-2001; 2001US-029575P

12-UNI-2001; 2001US-0299573P

12-UNI-2001; 2001US-0299573P

13-UNI-2001; 2001US-0299539P

14-UNI-2001; 2001US-0299539P

15-UNI-2001; 2001US-0299539P

21-UNI-2001; 2001US-0299539P

21-UNI-2001; 2001US-0300177P

26-UNI-2001; 2001US-0300159P

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28-UNI-2001; 2001US-035912P

28-UNI-2002; 2002US-0359035P

29-FEB-2002; 2002US-0359035P

21-FEB-2002; 2002US-0359035P

22-FEB-2002; 2002US-0359035P

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22-FEB-2002; 2002US-0359035P

22-FEB-2002; 2002US-0359035P

23-FEB-2002; 2002US-0359035P

24-FEB-2002; 2002US-0359035P

25-FEB-2002; 2002US-0359035P

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11-MAR-2002; 2002US-0359035P
        18-JUN-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antidiabetic; anorectic; cerebroprotective; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002WO-US017443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO:
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Query Match
Best Local Similarity
Matches 237; Conserv
                                                                                                                                           The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NoVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the
                                                                                                      Sequence 272 AA;
                                                                                                                                      polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 226; 772pp;
                                                                                                                                                                                                                                                                                                                                                                           or CNS diseases.
                                                                                                                                                                                                                                                                                                                                                                              New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ort T, Padigaru M, Patturajan M,
Rothenberg ME, Shenoy SG, Shimket
Spytek KA, Stone DJ, Vernet CAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dipippo VA,
Gerlach VL,
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DB; ADC10203.
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A, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
L, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda
NV, Li Liu X, Malyankar UM, Miller CE, Millet I;
adigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
g ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
y Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                Conservative
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                                             74.4%;
88.4%;
                            12;
                            Score 1232; D
Pred. No. 5.1e
12; Mismatches
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Rieger DK;
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                                              18-NOV-2004
                                                                  ADR86553;
                                                                                  ADR86553 standard; protein; 229
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                                                                                                                                  LOOIGGCSVTVPANVORWMRSCENLAPF
                                                                                                                                                    LOQTGGSSGAAPTNVQRWLKSCENLAPF
                                                                                                                                                                     HNAVNATLIDSWVDÍAI FOLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSV
                                                                                                                                                                                 HNAVTLTLIDSWVDIAMFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSV
                                                                                                                                                                                                         LIKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQK
                                                                                                                                                                                                                     LVKCFGEQARKOSRHEYQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQK 224
                                                                                                                                                                                                                                              TLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPEN
                                                                                                                                                                                                                                                                                     QEESNISIQALESRODDILKRIYELKAAVDGLSKMIQTPDADLDVTNIIQADBPTTLTTN
                                                                                                                                                                                                                                                                                                QETSEPSLQALESRQDDILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATN
                                            (first entry)
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p38/JTV-1; Cytostatic; cancer; leukemia; anticancer 84-312 amino acid sequence of p38/JTV-1 protein.

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RESULT 7
ADR86552
ID ADR8
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AC ADR8
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DT 18-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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E
                18-NOV-2004
                                                    ADR86552;
                                                                                      ADR86552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; SEQ ID NO 6; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-627822/61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-SEP-2003; 2003EP-00020344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park B;
                                                                                                                                                                                                                                                                         MCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIAMFQLREGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                                                                                      ERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQMKFSVQT
                                                                                                                                                                                                                                                                                                                                                                                                DADLDVINI I QADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                               GKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQRWMRSCENLAFF 229
                                                                                                                                                                                                                 GRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQRWLKSCENLAFF 312
                                                                                                                                                                                                                                                    MCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSMNSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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               (first entry)
                                                                                    protein; 161
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88.2%; Pred. No. 2.6e-1
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?.6e-101;
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RESULT 8
ABP01502
ID ABP0
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AC ABP0
XX
DT 24-J
XX

ABP01502; ABP01502

standard; protein;

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120 60 6

24-JUN-2002

(first entry)

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                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 143
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-2003; 2003EP-00020344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-161 amino acid sequence of p38/JTV-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-2003; 2003KR-00013058
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                                                                                                                                                                                                                                                              Match 44.4%;
Local Similarity 88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-627822/61.
121
                                      121
                                                                                                                                                                                                                                           143;
                                                                              61
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                                                                                                                                                                                                   1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                                                                                                                                                                                                                                                                                              161
                                                                                                       DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK
                       DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5; 47pp; English
  DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSV
                                                                              DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADBPTTLTTNALDLNSVLGKDYGALK
                                                                                                                                                             MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                            Score 735; DB 8;
Pred. No. 4.4e-67;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                 DB 8; Length 161;
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                                                                                                             Query Match
Best Local &
                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disorder; psorissis; benigh tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX protein sequence SEQ ID NO:2986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Tab in the specification). ABN15762 to ABN27222 encode the human ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2986; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-)
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                reperfusion injury in various tissues and conditions resulting from reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-106308/14.
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                                                                                                                  Similarity
                                                                                                                                                                                       51
                             DGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALKDIVI 124
DGLSKMIHTPDADLDVTNILQADEPTTLTTNALDLNSVLGKDYGALKDIVI
                                                                                                                                                                                       Ą
                                                                                            Conservative
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                                                                                            0
                                                                                                                     Score 248;
Pred. No. 1
                                                                                                 Mismatches
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                                                                                                                     DB 5; Length 51; .3e-17;
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              51
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RESULT 9 ABB62468

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VFRSMNSALGRSPWLVGNELTVADVVLWSVL 285

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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 14196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB62468 standard; protein; 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 14196; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
N-PSDB; ABL06571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                Local Similarity
216 ISSPTMYVDIYGEVNIIRYLGRVGPAEYRYEGSPLCNEIDLVLDICYQLLRCNTHKTQVA
                                                             162
                                                                                       145 RYRVLSTVHTHSSVKNV-----PENLVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQM
                                                                                                                                                                            58 RTGRNAATCALDLDSLGRQIQRLLKDDTASVAARQEKVLKQLEELKAQLGQIR-----
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                                                                                                                                                ADLDVINILQADEPTILATNILDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCE 144
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                            KPSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTL---IDSWVDIAMFQLREGSSKEKAA
                                                             LYTIDVKTFTHSTMADIGPAAREFEANLAKVPVNPALP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                   Score 216.5; DB 4
Pred. No. 4.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EW;
                                                                                                                       -GLKEVPLQDVVINGHPNFIPYALLALKNAWRN 161
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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	767	559	559	448	434	434	959	789	789	789	519	515	475	360	1057	646	443
US-09-249-016-10598 US-09-248-796A-18678 US-09-428-156B-2 US-09-428-156B-2 US-09-328-352-5379 US-09-328-352-6379 US-09-543-681A-6505 US-09-543-681A-6505 US-09-59-477-84 US-10-099-285A-84 US-09-543-681A-6879 US-09-120-601-6 US-09-120-601-6 US-09-120-601-6 US-09-120-601-6 US-09-120-601-1 US-09-821-016-1 US-08-836-567-8	w	4	4	w	w	ω	4.	4	4	w	4	4	4	4.	4	4	4
	US-08-836-567-8	US-10-266-787-1	US-09-821-016-1	US-09-120-601-6	US-09-120-601-4	US-09-012-072-4	US-09-543-681A-6879		US-09-589-477-84	US-09-002-285-84	US-09-543-681A-6505	US-09-489-039A-8208	US-09-328-352-5379	US-09-949-016-10589	US-09-428-156B-2	US-09-248-796A-18678	US-09-949-016-10598
	8, Appli	1, Appli	1, Appli	6, Appli	4, Appli	4, Appli	6879, Ar	84, Appl	84, Appl	84, Appl	6505, A	8208, Ap	5379, A	10589, 7	2, Appli	18678, 1	FASOT

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Sequence 11312, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICATT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF INTILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11312
LENGTH: 341
TYPE: PRT
ORGANISM: Human
US-09-949-016-11312
Query Match
Best Local Similarity 87.2%; Pred. No. 9e-153;
Matches 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;
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US-09-949-016-11312

ALIGNMENTS

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241

MPQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ

60 81 120 141 180 201 240 261

IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQ

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RWLKSCENLAPFSTALQLLK 320

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61 DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK

DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK

DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVVPENLVKCFGEQARKQSRHB

YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA

YOLGETLIWKNVPKTOMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA

1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD

HHYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD

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US-08-518-862C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.8%; Score 1436; DB 2; Best Local Similarity 87.5%; Pred. No. 9.6e-150; Matches 273; Conservative 14; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PAtentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/518,862C

EILING DATE: 24-AUG-1995

CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.49697
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Nicolaides, Nicholas C.
TITLE OF INVENTION: Human JTV1 Gene Overlaps PMS2 Gene
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Banner & Witcoff, Ltd. STREET: 1001 G Street, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                          241 MFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ 300
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                                     301
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                                                                                                                                                                                                                                        121 DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHE 180
                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                             61 DILKRLYELKAAVDGLSKMIQTPDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK
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o. 5843757
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                                                                                                                                                                                                                                                                                                                                                                                                    1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                                                                                                                                                                                  DIVINANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
                                                                                                                                                                                                                                                                                                                                                                    RWMRSCENLAPF 312
                                 RWLKSCENLAPF 312
                                                                   IFQLKEGSSKEKAAVFRSMNSALGKSPWLAGNELTVÅDVVLWSVLQQIGGCSVTVPANVQ 300
                                                                                                                                         YQLGFTLIWKNVPKTQMKFSIQTMCPIEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIA 240
                                                                                                                                                                   YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA 240
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RWMRSCENLAPFNTALKLLK
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CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60/093,530
EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
SEQ ID NO 37
LENGTH: 1440
TYPE: PRT
ORGANISM: Homo sapiens
US-09-357-251-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION

APPLICANT: Cunningham, Mary Jane
APPLICANT: Zweiger, Gary
APPLICANT: Kaser, Matthew R.
APPLICANT: Kaser, Matthew R.
APPLICANT: Penzer, Scott
APPLICANT: Seilhammer, Jeffrey J.
APPLICANT: Seilhammer, Jeffrey J.
APPLICANT: Baughn, Mariah
APPLICANT: Hail, Preeti
APPLICANT: Lal, Preeti
TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
CURRENT APPLICATION NUMBER: US/09/443,184A
CURRENT FILING DATE: 1999-11-19
KONTMADE, DEED BOOKS: 138
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US-09-443-184-48
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/09357251
Patent No. 6271441
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PERL Program SEQ ID NO 48
LENGTH: 1512
                                                                                                                                                                                                                                                     APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
FILE REFERENCE: BB-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.4%;
Best Local Similarity 21.8%;
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 KKAPVHVKRWFGFLEAQQAFQS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 GAAPTNVQRWLKSCENLAPFST 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 DIAMPQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQ-----QTGGSS 292 : : : | | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 INANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHEYQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 GFTLIWKNVPKTOMKFSVQTMCPIEGEGNIARFL----FSLFGQKHNAVTLTLIDSWV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 EFSATKL--SSCDSFTSTINELNHCLSLRTYLVGNSLSLADLCVWATLKGNAAWQEQLKQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LTVNSGDPPLGALL---------AVEHVKDD-VSISVEEGKENILH----
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6372431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 3; Length 1512; Pred. No. 0.096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
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Mon Feb 28 10:03:53 2005
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Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
Published Applications AA:*

1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2-6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2-6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2-6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

7: /cgn2-6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

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13: /cgn2-6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

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15: /cgn2-6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2-6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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18: /cgn2-6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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19: /cgn2-6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

20: /cgn2-6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1380268 seqs, 327241040 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPMYQVKPYHGGSAPLRVEL.....RWLKSCENLAPFSTALQLLK 320
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2084.158 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
1436 1069 735 105.5 103.5 99.5 99.5 96.5 96.5	Score
804 04400000000000000000000000000000000	Query Match Length DB
312 229 161 925 980 914 691 1440 1440 722	ength I
16 16 16 16 16 16 16 16 16 16	. B
US-10-463-676-4 US-10-463-676-6 US-10-463-676-5 US-10-463-676-5 US-10-437-963-126132 US-10-369-493-6336 US-10-424-599-260388 US-10-437-963-153870 US-10-282-122A-44369 US-09-815-242-5841 US-09-864-464-37 US-10-369-493-10013	ID
Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 12612; Sequence 26036, Ap Sequence 26038, Sequence 15870, Sequence 15870, Appl Sequence 37, Appl Sequence 37, Appl Sequence 31, Appl Sequence 123904, Sequence 10013, A	Description

45	44	43	42	41	40	39	38	37	36	35	34	u u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
88.5	88.5	89	89	89	89	89	89	89	89	89.5	90	90	90	90	90	90	90	90	90	90.5	90.5	90.5	90.5		91	91	91	91	93		93.5
5.3	5.3	5.4	5.4	5.4	5.4	5.4		5.4		5.4		5.4	5.4	5.4	5.4	5.4	5.4	•	5.4				ა ა							5.6	6
799	656	1057	1056	1056	1056	1056	1056	1056	407	203	5215	5215	5215	5215	5215	1500	856	856	559	716	661	578	419	1788	1319	805	455	201	1398	204	456
16	15	16	17	17	17	15	5	15	15	15	14	10	5	9	9	16	9	9	9	15	15	15	15	16	16	15	15	15	16	15	15
US-10-437-963-112603	US-10-369-493-18559	0	US-10-600-009-476	US-10-600-009-474	0-600-	US-10-282-174-476	US-10-282-174-474	÷	-10-424-		0-271-8	US-09-836-821-2	US-09-988-384B-2	US-09-860-846-2	US-09-861-289-2	US-10-437-963-111265	US-09-364-847-35	US-09-364-847-33	US-09-364-847-21	US-10-369-493-2175	÷	10-418-8	-10-424-5	-10-437-9	-10-437-963	-10-424-5	-10-425-114	US-10-369-493-13717	US-10-437-963-180124	-10-369-493-	US-10-425-114-63166
Sequence 112603,			Sequence 476, App	Sequence 474, App	e 472,	e 476,	e 474,	æ	æ	e 860	e 45, Ap	2, 1	e 2,	2, 7	N	Ø	Sequence 35, Appl	Sequence 33, Appl	N		e 2556	æ	e 2603	Sequence 197780,	Ø	æ	æ	Seguence 13717, A	O		Sequence 63166, A

ALIGNMENTS

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                                                                                                                                                                                                                                                                 ; FEATURE;
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(312)
; OTHER INFORMATION: 1-312 amino acid sequence of p38/JTV-1
US-10-463-676-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-463-676-4
; Sequence 4, Application US/10463676
; Publication No. US20040175375A1
; GENERAL INFORMATION:
                                                                                                                                                                  Query Match
Best Local Similarity 87.5
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 312
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Park, Bum-Joon
TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating Cancer
FILE REFERENCE: 012679-091
CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: KR 10-2003-13058 PRIOR FILING DATE: 2003-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kim, Sunghoon APPLICANT: Park, Bum-Jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
61 DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK 120
                                                                                                      1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD
                                                                           MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                                                     86.8%; Score 1436; DB 16; Length 312;
87.5%; Pred. No. 2.6e-137;
tive 14; Mismatches 25; Indels 0
                                                                                                                                                                  0,
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                                                                                60
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US-10-463-676-5
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US-10-463-676-6
; Sequence 6, Application US/10463676
; Publication No. US20040175375A1
; Publication No. US20040175375A1
                                                                                                 RESULT 3
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Sequence 5, Application US/10463676
Publication No. US20040175375A1
GENERAL INFORMATION:
APPLICANT: Kim, Sunghoon
APPLICANT: Park, Bum-Joon
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Best Local S
Matches 202
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NAME/KEY: PEPTIDE
'COMPTON: (1)...(2
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LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kim, Sunghoon
APPLICANT: Park, Bun-Joon
TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating
FILE REFERENCE: 012679-091
CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 84-312 amino acid sequence p38/JTV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                            264
                                                                                                                                                                                                                     204 MCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIAMFQLREGSSKEKAAVFRSNNSAL
                                                                                                                                               181
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                                                                                                                                                            GRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQRWLKSCENLAPF 312
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                MCPTEGEGNIARFLFSLFGQKHNAVNATLIDSWVDIAIFQLKEGSSKEKAAVFRSWNSAL
                                                                                                                                                                                                                                                           EHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQDYQLGFTLIWKNVPKTQMKFSIQT
                                                                                                                                                                                                                                                                                ERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQMKESVQT
                                                                                                                                                                                                                                                                                                                                           DADLDVTNILQADEFITLATNTLDLNSVLGKDYGALKDIVINANFASPFLSLLVLHRLLC 143
                                                                                                                                       GKS PWLAGNELTVADVVLWSVLQQIGGCSVTVPANVQRWMRSCENLAPF
                                                                                                                                                                                                                                                                                                                         DADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQLGFTLIWKNVPKTQMKFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTLIDSWVDIA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DÍVÍNANPASPPLSLLVLHRLLCEHFRVLSTVHTHSSVKSVPENLLKCFGEQNKKQPRQD
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          64.6%;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 1069; DB 10;
Pred. No. 4e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length
                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                                                                      Matches
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53221)B; CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14; NUMBER OF SEQ ID NO 126132
LENGTH: 925
TYPE: ppm
                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_28709C.1.pep US-10-437-963-126132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-437-963-126132
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                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 126132, Application US/10437963 Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 143; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1
TITLE OF INVENTION: for Screening Pharmaceutical Composition f
FILE REFERENCE: 012679-091
CURRENT APPLICATION NUMBER: US/10/463,676
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR APPLICATION NUMBER: KR 10-2003-13058
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 161
TYPE: PRT
ORGANISM: Homo f
                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
LOCATION: (1)...(161)
OTHER INFORMATION: 1-161 amino acid sequence of p38/JTV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DIVINANPASPPLSILVLHRILCERYRVLSTVHTHSSVKNV 161
83 PDADLDVINILQAD--EPTTLATNTLDLNSVLGKDYGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DILKRLYBLKAAVDGLSKMIQTÞDADLDVTNIIQADEPTTLTTNALDLNSVLGKDYGALK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK 120
                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                             YMVDNIIAKVTGPV-----TIDPRLQALYKKTTELVGIEKQSEKLVKILSLGDDVHA
                                                                                                     YRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQDDI--LKRLYELKAAVDGLSKMIHT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQEESNLSLQALESRQD
                                                                                                                                               6.4%; Score 105.5; DB 16; llarity 20.3%; Pred. No. 0.51; Conservative 46; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 161;
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                        127
                                                                  203
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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Copyright (c) 1993 - 2005 Compugen Ltd
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T142977
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ketol-acid reducto transcription fact translation elonga structural mainten ras-associated prohypothetical prote transcription init probable glutamate translation elonga poly (3-hydroxyalka kinesin-related prhypothetical prote genome polyprotein
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4 5	44	43	42	41	40	9	38	37	36	35	34	33	32	31	30
86	87	87.5	87.5	88	88	88	88.5	88.5	89	89	89	89	69	•	89.5
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	hypothetical prote	ATP-dependent heli	hypothetical prote	acetyl-CoA carboxy	acetyl-CoA carboxy	hypothetical prote	acetyl-CoA synthet	gtp-binding protei	interphotoreceptor	kinesin-like spind	neural zinc finger	penicillin-binding	glutathione S-tran	peptide synthetase	multifunctional am

ALIGNMENTS

RESULT 1 T52043

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A;Introns: 25/3; 215/2; 266/3; 540/3; 585/3; 786/1; 898/2 C;Superfamily: insulin-degrading enzyme (IDE) C;Keywords: hydrolase; metalloproteinase; zinc F;70,74/Binding site: zinc (His) #status predicted F;73/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable zinc proteinase (EC 3.4.24.-) C02G6.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T30089
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T30089
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A;Map position: 5
A;Map position: 5
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
F;223-499/Domain: glutamine-tRNA ligase homology <EGL>
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Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 YASV-FSSGSEFENAC--GRVDKYLESSTFLVGHSLSIADVAIWSALAGTG------
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KMKKYENALKTSHHALHLPEKN--EYIATNFGQKPRESVKNEHPKLISDDGWSRVWFKQD 503
                                                                            LTKYEPERIKELLSTLTPSN-----MLVRVVSQKFKEQEGNTNEPVYGTEMKVTDISPE
                                                                                                                                                                                              ---LKAAVDGLSKMIHTPDADL-DVT-NILQADEPTTLATNT-----LDLNSVLGKDY- 116
                                                                                                                                                                                                                                   HKGPGSLLVELKRLGW-VNSLKSDSNTIAAGFGILNVTMDLSTGGLEN-VDEIIQLMLNY 333
                                                                                                                                                                                                                                                                           HGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQDDILKRLYE-
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                                     --VLSTVH--THSSVKNVPENLVKCFGEQARKQSRHEYQL-----GFTLIW----
                                                                                                                                                                                                                                                                                                                                             6.3%;
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Pred. No. 0.29
22; Mismatches
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ДЪ	B &	D Q	Db Qy	Qy dd	Qу	Quer Best Matcl	RESULT B89797 glycero C;Speci C;Speci C;Acces R;Kurod ma, A.; C;Sh Lancet A;Title A;Title A;Refer A;Acces A;Statu A;Moleci A;Residd A;Cross A;Exper C;Super; C;Super;	Db Qy	g &	dg Qy	D Qy
250 KEKAAVERSMISALGRSPWLVG 271 : ::	210 EGNIARFLESLEGOKHNAVTUTLIDSWVDIAMFQLREGSS 249 : :: ::	. a w	102 ATNTLDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNV 161 	53 QALESRODDILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADSPTTL 101 ::::	1 MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSL 52 :	Query Match 6.0%; Score 99; DB 2; Length 691; Best Local Similarity 20.2%; Pred. No. 3.4; Matches 65; Conservative 53; Mismatches 110; Indels 94; Gaps 15;	RESULT 4 B89797 glycerol ester hydrolase [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: B89797 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Residues: preliminary A;Molecule type: DNA A;Residues: 1-691 <kuip- a;cross-references:="" c;superfamily:="" gb:ba000018;="" gspdb:g.;superfamily:="" lipase="" lipase<="" pid:g13700235;="" pidn:bab41533.1;="" staphylococcus="" td="" triacylglycerol="" unifrot:099w06;=""><td>309 LAPFSTAL 316 </td><td>252 KAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQRWLKSCEN 308 </td><td>221 FGQKHNAVTLTLIDSWVDIAMFQLREGSSKE 251 </td><td>190KNVPKTQMKFSVQTMCPIEGBGNIARFLFSL 220 </td></kuip->	309 LAPFSTAL 316 	252 KAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSSGAAPTNVQRWLKSCEN 308	221 FGQKHNAVTLTLIDSWVDIAMFQLREGSSKE 251	190KNVPKTQMKFSVQTMCPIEGBGNIARFLFSL 220

RESULT 5
G92441
G92441
C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

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Regult
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=FVB/N, and

Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

RX STRAINS-FYB/N, and FVB/N-3; TISSUE-Mammary tumor;
RX MEDIINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Gavcla A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
RA Richards S., Morley K.C., Hale S., Gavchenko Y., Bouffard G.G.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Miting M., Madan A., Tones S., Gavchenko Y., Bouffard G.G.,
RA RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Rodriguez G. T. Marra M.A.

Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024410; AAH224410.1; -.
EMBL; BC026972; AAH26972.1; -.
MGD; MGI:3285237; Jtv1.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR01987; GST_C_1ike.
Pfam; PF00043; GST_C; 1.
SEQUENCE 320 AA; 35396 NM; 1745D7EE4BC3670D CRC64;

SEQUENCE FROM N.A. STRAIN=FVB/N-3; TISSUE=Mammary tumor;

Strausberg Submitted

(MAR-2002)

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mmary tumor. C3;
the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Mammary tumor.

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					P10335	Q8btr1	Q8v9a2	026161	Q9km05	Q7a7p2	Q99wq6	Q798z7	Q6gcf1	Q8nyc2	Q8rq67	Q6tem5	Q8k2j4	Q8d7u3	
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RM MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RM Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Stapleton M., Soares M.B., Foshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Altards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S., Lordinan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holting M., Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzyminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Mara M.A.,

"Grocett L.D., Schemutz J., Myers R.M., Schein J.E.,

"Grocett L.D., Schemutz J., Myers R.M., Schein J.E.,

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Q8R2Y6;
01-JUN-2002
01-JUN-2002
01-MAR-2004
Strausberg R.;
Submitted (APR-2002)
EMBL; BC026958; AAH2
                                                                                         STRAIN-CZECH II; TISSUE-Mammary
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Mus musculus (Mouse) .

Mus musculus (Mouse) .

Metazoa; Chordata;

Metazoa; Rodentia;
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                                                                                                                                                                                                                   sequences.";
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                                EMBL/GenBank/DDBJ databases
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Pred. No. 2.6e-128;
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thi; Muridae; Murinae; Mus
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Best Local S
Matches 319
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99066915; PubMed=9878398; DOI=10.1006/jmbi.1998.2316; Quevillon S., Robinson J.-C., Berthonneau E., Siatecka M., Mi "Macromolecular assemblage of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characteri a core protein."; J. Mol. Biol. 285:183-195(1999).
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Multisynthetase complex auxiliary component p38.
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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InterPro; IPR010987; GST_C like.
Pfam; PF00043; GST_C; 1.
SEQUENCE 320 AA; 35423 MW; 1
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                                                                                                                                                                     SUBUNIT: Component of the multisynthetase complex which is COMPONENT: Component of the multisynthetase comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxil proteins, p18, p48 and p43.

SIMILARITY: Contains 1 GST-like domain.
                                                                                                                                                                                                                                                                                                                                                                                that serves as a template for the structure
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ilarity 99.7%;
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Pred. No. 4
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Q13155; Q9P1L2;
Q1-NOV-1997 (Rel
16-OCT-2001 (Rel
TISSUB-Lymph;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hisleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.

Stapleton M.J., Usdin T.B., Toshiyaki S., Carninci P., Prange C.,

Stapleton M.J., Usdin T.B., Toshiyaki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP072727; AAD38422.1; -.
InterPro; IPR010987; GST C like
InterPro; IPR004046; GST Cterm.
Pfam; PP00043; GST C; 1.
Protein biosynthesis.
SEQUENCE 320 AA; 35433 MW;
                                                                                                                                                                                                          MEDLINE-96115582; PubMed-8666379;
Nicolaides N.C., Kinzler K.W., Vogelstein B.;
"Analysis of the 5' region of pMS2 reveals he
and a novel overlapping gene.";
Genomics 29:329-334(1995).
                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Multisynthetase complex auxiliary component p
                                                                                                                                                                                 SEQUENCE
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Primates;
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Pred. No. 1.
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1.6e-121;
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                                                             Scheetz T.E.,
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61 61

DILKRLYELKAAVDGLSKMIQTPDADLDV

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MPMYQVKPYHGGSAPLRVELPTCMYRLPNVHSKTTSPATDAGHVQETSEPSLQALESRQD

Similarity

1.6e-112;

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121

DIVINANPASPPLSLLVLHRLLCERYRVLSTVHTHSSVKNVPENLVKCFGEQARKQSRHE

DILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATNTLDLNSVLGKDYGALK MPMYQVKPYHGGGAPLRVELPTCMYRLPNVHGRSYGPAPGAGHVQBESNLSLQALESRQD

/TNIIQADEPTTLTTNALDLNSVLGKDYGALK

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Query Match
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Matches 279
                                                                                 InterPro; IPRO10987; (InterPro; IPRO04046; GPfam; PF00043; GST C; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22716800; PubMed=12819782; DOI=10.1038/ng1182; Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Lee S.W., Han J.M., Lee H.-W., Kim S.; "Downzegulation of FUSE-binding protein and c-myc by tR cofactor p38 is required for lung cell differentiation. Nat. Genet. 34:330-336 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full
                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercise
                                                                                                                                                                                    EMBL; U24169; AAC50391.1; ALT_FRAME.
EMBL; BC002853; AAH02853.1; --
EMBL; BC10156; AAH10156.1; --
EMBL; AF116615; AAF71039.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                   H-InvDB;
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                                                                                                                                                                                                                                                                                                                                                                                       the proteasome.

the proteasome.

SUBUNIT: Component of the multisynthetase complex which is SUBUNIT: Component of the multisynthetase comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, and aspartyl-tRNA synthetases as well as three auxil proteins, pl8, p48 and p43. Binds FUBP1.

SIMILARITY: Contains 1 GST-like domain.

CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Probable core protein of the multisynthetase that serves as a template for the assembly of the suprastructure. Mediates ubiquitination of FUBPl and its deg
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                                                                  biosynthesis
E 320 AA;
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-J., Kang Y.-S., Kim H.J., Park J.-H.,
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GST_Cterm.
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Score 1464; DB
Pred. No. 1.6e-1
6; Mismatches
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Y., Bouffard
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

WA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

WA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

WA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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WA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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WA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

WA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

WA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

WA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

WA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

WA Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

WA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

WA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

WA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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SEQUENCE
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casawant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casawant T.L., Scheetz T.E.,

RA Stapleton M., Joudin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rohas S.A., Mozwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Mozwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

PA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Knama S.T. Marra M A.;
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                                                                                                                SEQUENCE
                                                                                                                                                                                                              Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary
                                                                                                            InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C like.
Pfam; PP00043; GST_C; 1.—
Pfam; PP00043; GST_C; 1.—
SEQUENCE 280 AA; 31097 MW; E
                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                             "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                       Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Jtv1;
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                    ; BC024480; AAH24480.1;
MGI:2385237; Jtv1.
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                                                        Similarity
QETSEPSLQALESRQDDILKRLYELKAAVDGLSKMIHTPDADLDVTNILQADEPTTLATN
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                                                  Score 1412; DB 2; pred. No. 2.6e-108;
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Last annotation update)
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Kilausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Scheefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Fsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Fsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Fsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Fsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Fsieh F.,

A Stapleton M., Gares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Stapleton M., Gulin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Tuchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kornes G. T. Wang A.C., Smailus D.E., Schnerch A., Schein J.E.,

Kornes G. T. Makek U., Smailus D.E., Schnerch A., Schein J.E.,
                         Query Match
Best Local S
Matches 216
                                                                                                                                      Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/G
EMBL; BC074561; AAH74561.1; -.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
                                                                                                                                                                                                                                                                   SEQUENCE PROM N
TISSUE-Embryo;
Klein S., Gerha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6DK86;
                                                                                                                                                                                                                                                                                                                                                                 Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
"Generation and initial analysis of and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus tropicalis (Western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGC69221 protein.
Name=MGC69221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
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                           Conservative
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                                                                                                                       34480 MW;
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Last annotation updat
                                                Score 1153.5; DB 2; Length 311; Pred. No. 6.8e-87;
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                                                                                                                                                                                                                                                                                                                                  RX MEDLINE=2238/257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Arnes S. T. Marra M.A.
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Q6INU4;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                Klein S.L., Strausberg Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGC80304 protein.
Name=MGC80304;
                                                                                                                                                MEDLINE=22341132;
                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                            Jones S.J., Marra M.A., "Generation and initial analysis and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                initiative.";
                                                                    Genetic and genomic tools for
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                           225:384-391 (2002)
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                                                                                                                                                   PubMed=12454917;
                                                                                                                       R.L.,
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Last annotation update)
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                                                                         Xenopus
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                                                                                                                       DOI=10.1002/dvdy.10174; r L.. Pontius J., Clifton S.W.,
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RESULT
Q7ZYD7
RX MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsteh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsteh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McErana N.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., McErana N.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
NA Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,
NA Jones S.J., Marra M.A.;
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01-JUN-2003
01-MAR-2004
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Submitted (JUN-2004) to the EMBL/G
EMBL; BC072178, AAH72178.1; -.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C like.
Pfam; PF00043; GST_C, 1.-
SEQUENCE 311 AA; 34424 MW; D5E
                                                                                                                                                                                                                                                                                                                                                       Urima — protein.
Jtv1-prov protein.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Ver
Bukaryota; Metazoa; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7ZYD7
Q7ZYD7;
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TISSUE=Ovary;
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ia; Pipoidea; Pipidae;
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Matches 218
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01-OCT-2003
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SEQUENCE FROM N.A.
TISSUB-Kidney;
MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
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Submitted (JAN-2003) to the EMBL/(
EMBL; BC043832; AAH43832_1; -.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
Pfam; PF000043; GST_C; 1.
SEQUENCE 311 AA; 34647 MW; 2F0
                                                                                                                                                                                                                             Zgc:63976.
ORFNames=zgc:63976;
Brachydanio rerio (
                                                                                                                                                                       Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                     NCBI_TaxID=7955;
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KWMKSCENLASFKSVLRFLK
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Strausberg R.L., Wagne
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Teleostei; Ostariophysi;
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44; Mismatches
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Best Local Similarity
Matches 188; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053178; AAM53178.1; -
ZFIN; ZDB-GENE-040426-2652; zgc:63976.
InterPro; IPR004046; GST Cterm.
InterPro; IPR004046; GST Cterm.
InterPro; IPR004046; GST Cterm.
Pfam; PF00043; GST C; 1.
Pfam; PF00043; GST C; 1.
BABF6B951208244A CRC64;
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                                                                                                                                                                             Q7Q7A3 PRELIMINARY; PRT; 340 AA. G7Q7A3; CTEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last sequence up 01-MAR-2004 (TrEMBLrel. 26, Last annotation 10-MAR-2004 (TrEMBLrel. 26, Last annotation AgCP5808 (Fragment).
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   SEQUENCE FROM N.A.
                                                                                  Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins
Neoptera; Endoptorygota; Diptera; Nematocera;
                                                     NCBI_TaxID=180454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDSWVDIAMFQLREGSSKEKAAVFRSMNSALGRSPWLVGNELTVADVVLWSVLQQTGGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPMYQVKPV--SPADITVDLPTCMYKLPNVHAQGASLGEHALQNGEV----DPTVKALEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SAPANVQRWLKSCQNLGYPSCVDPLLQ
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Pred. No. 4.1e-68;
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annotation update)
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                                                                                     Insecta; Pteryg
era; Culicoidea;
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                                                                                                              Pterygota,
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                                                                                           Anopheles
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REDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hookins R.A., Galle R.F., RA Adams M.D., Celniker S.E., Li P.W., Hookins R.A., Galle R.F., RA Adams M.D., Scherer S.E., Li P.W., Hookins R.A., Galle R.F., RA Adams M.D., Scherer S.E., Li P.W., Hookins R.A., Galle R.F., RA Adams M.D., Chemp. M., Feiffer B.D., RA Stitton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Feiffer B.D., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Feiffer B.D., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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Best Local S
Matches 94
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Q7KUM5;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG12304-PB.
ORFNames=CG12304;
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Submitted (MAR-2002) to the EMBL/GenBack/DDBJ databases.
-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PEST;
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(TrEMBLrel.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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No. 6.
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Query Match
Best Local S
Matches 86
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A Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHson D.R., Nelson K.A., Nixon K., Musskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodagr, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
The genome sequence of Drosophila melanogaster.";
RN [2]
                                                                                                                                                        SEQUENCE F
FlyBase;
Submitted
                                                                          SEQUENCE
                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12537572;
Milsra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stappleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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(Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.

(Celniker S.E., Hodgson A., Dayan S.P., Frise E., Hodgson A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

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                                                                               EMBL; AE003530; AAS64998.1; -.
InterPro; IPR004046; GST_Clerm.
InterPro; IPR010987; GST_C_like.
Pfam; PF00043; GST_C; 1.
PFAM; PF00043; GST_C; 1.
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"The transposable elements of the Drosophila me
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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EMBL; AY069537; AAL139682.2; -.
FlvBase; FBgn0036515; CG12304.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8T060;
01-JUN-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Eukaryota; Metazoa; Arthropoda; Haxapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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ORFNames=CG12304;
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InterPro; IPR010987; GST_C_like
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                                                                                                                     MYQVKPYHGGSAPLRVELPTCMYRLPNV-----HSKTTSPATDAGHVQETSEPSLQA
KEVPLQDVVINGHPNFI PYALLALKNAWRNLYTI DVKTFTHSTMADIGPAAREFEANLAK
                                                  VAARQEKVLKQLEELKAQLGQIR-----
                                                                                                MYELKTL---LPQFDIKLPTCMYPLKNVSLAADSLASGSSTSASTSA---STSSCDDTAS
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Pred. No. 4.3e-10;
7; Mismatches 122;
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InterPro; IPR004046; GST_Cterm.
InterPro; IPR010987; GST_C_like.
Pfam; PP00043; GST_C; 1.
SEQUENCE 322 AA; 35528 MW; 8
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                                                                                                                                                                                                                                                                                                   EGSPLCNEIDLVLDICYQLLRCNTHKTQVAMVRLLDKRLQKQQYFGGSQMSVADVGVYSS
                                                                                                                                                                                                                                                                                                                                                                                                         VPVNPALP----KISVTLIWKNCEHTEMISSPTMYVPIYGEVNIIRYLGRVGPAEYRY
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Last annotation updat
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Pred. No. 4.5e-10;
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gealge R.A., Lewis S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.I., Harvey D.A., Heiman T.J., Herrandez J.R., Houck J.,
RA Harris N.I., Harvey D.A., Heiman T.J., Herrandez J.R., Houck J.,
RA Harris N.I., Harvey D.A., Heiman T.J., Hermandez J.R., Houck J.,
RA Hasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Mchallov G., Milshina N.V., Mobarry C., Morris J., Moshredi A.,
RA Melson D.R., Nelson K., Stapleton M., Strong R., Sun E.,
RA Molson D.R., Nelson K., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Vennter E., Wang A.H., Wang X.,
RA Spier B.C., Stdar-Kiamos I., Singson M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Vennter E., Wang A.H., Wang X.,
RA Harliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Schon X.H., Zhong F.N., Zhong W., Zhong W., Zhon X., Smith H.O.,
RA Schone S., The S., Zhong W., Zhong W., Zhou X., Smith H.O.,
RA Schone S., The S., Zhong W., Zhong W., Smith H.O.,
RA Schone S., Zhong W., Zhong W., Zhou X., Smith H.O.,
RA Schone S., Shong R., Zhong W., Zhou X., Smith H.O.,
RA Schone S., Shong R.,
                                                                                                                                                                                                                                                                                    MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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25-JAN-2005 (Rel. 46, Last annotation update)
Probable multisynthetase complex auxiliary component p38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENOME REANNOTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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                                                                                                                                                                                                                                                                          Lewis S.E.;
                                                                                                                                                                                                                                                     Annotation of the
comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetase as well as three auxiliary proteins, pl8, p48 and p43 (By similarity).

SIMILARITY: Contains 1 GST-like domain.
                                                                                                                                                                                                                                                   Drosophila melanogaster
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Search completed: February 23, 2005, 13:57:15 Job time: 61.9811 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003530; AAF49612.1; -.
IntAct; Q9VUR3; -.
FlyBase; FBgm0036515; CG12304.
InterPro; IPR010987; GST_Clike.
InterPro; IPR0104046; GST_Cterm.
Pfam; PF00043; GST_C; 1.
Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE 334 AA;
                                                                    276 MVRLLDKRLQKQQYFGGSQMSVADVGVYSSL 306
                                                                                                    255 VFRSMNSALGRSPWLVGNELTVADVVLWSVL 285
                                                                                                                                       216 ISSPTMYVPIYGEVNIIRYLGRVGPAEYRYEGSPLCNEIDLVLDICYQLLRCNTHKTQVA
                                                                                                                                                                         198 KFSVQTMCPIEGEGNIARFLFSLFGQKHNAVTLTL---IDSWVDIAMFQLREGSSKEKAA 254
                                                                                                                                                                                                             162 LYTIDVKTFTHSTMADIGPAAREFEANLAKVPVNPALP-----KISVTLIWKNCEHTEM
                                                                                                                                                                                                                                               145 RYRVLSTVHTHSSVKNV------PENLVKCFGEQARKQSRHEYQLGFTLIWKNVPKTQM 197
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                                                                                                                                                                                                                                                                                                                                                          AGLGVCG--KTFQHTTAFQNG------GLKEVPLQDVVINGHPNFIPYALLALKNAWRN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                MYELKTL----LPQFDIKLPTCMYPLKNVSLAADSLASGSSTSASTSASTSSCKLEANRID
                                                                                                                                                                                                                                                                                                                        ADLDVINILQADEPTILATNILDLNSVLGKDYGALKDIVINANPASPPLSLLVLHRLLCE 144
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36933 MW; B68FD70AE621990F CRC64;
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seq length: 2000000000
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ALIGNMENTS

RESULT 1 AAY32501 ID AAY32501 AC AAY3 AC AAY3 AC AAY3 AC Huma XX Homc XX C1-1 DR N-PX XX C1a: XX C1a: XX C1a: XX Sequence CC the C AAY32501 standard; protein; 465 Human parkin gene variant protein. AAY32501; N-PSDB; AAX99923. Shimizu N, Mizuno Y; 09-FEB-1999; 12-AUG-1999. WO9940191-A1. Homo sapiens. 21-OCT-1999 WPI; 1999-494295/41. 09-FEB-1998; Parkinson's disease related gene; parkin gene; variant; gene therapy. (SHIM/) SHIMIZU N. (MIZU/) MIZUNO Y. (first entry) 98JP-00027531 99WO-JP000545 ₹

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MIVFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD

Query Match Best Local Similarity Matches 465; Conserv

Conservative

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Mismatches

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Gaps

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Length 465; Indels

100.0%; Score 2596; DB 2; 100.0%; Pred. No. 2.3e-219;

Sequence 465 AA;

This sequence is encoded by a gene of the invention, and is implicated in the pathology of Parkinson's disease. This sequence is a variant of the parkin gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and investigation of Parkinson's disease

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Gene implicated in the pathology of Parkinson's disease, used treatment of the disease.

Claim 1; Page 83-88; 114pp; English.

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                 New isolated nucleic acid sequence encoding a Parkin polypeptide, for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and iscreening assays.
                                                                       WPI; 2003-046812/04.
N-PSDB; AAD47679.
                                                                                                                                                29-MAR-2001; 2001DK-00000525.
03-APR-2001; 2001US-0281286P.
                                                                                                                                                                                                                                                                                          Human; Parkin protein; neurological disorder; apoptosis; gene therapy; ischaemic stroke; Parkinson's disease; Alzheimer's disease; nootropic; transgenic; cerebroprotective; neuroprotective; neurotransplantation.
                                                                                                                                                                               02-APR-2002; 2002WO-DK000221
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Best Local Similarity 100.0%;
Matches 465; Conservative 0
ABO07156 standard;
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Pred. No. 2.3e-219;
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                                                                                                                                                           ABO07156;
                                                                                                        p53
                                                                                                   modifying protein,
                                                                                                                                (first entry)
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antiapoptotic; p53 pathway; breast cancer; colon cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder. Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antianoptotic: p53 pathway; breast cancer; colon cancer; kidney canc

Claim

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Page 69;

71pp; English

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                                                                                                                                                                                                                                                                                                                                                     The invention relates to identifying (M1) a candidate p53 pathway condulating agent, by contacting an assay system comprising a purified HM completed (human orthologue of genes that modify the p53 pathway in cC Drosophila) or nucleic acid with a test agent under conditions, where but cfor the presence of the test agent, the system provides a reference cativity, and detecting a test agent, the system provides a reference contracting a cell defective in p53 pathway of a cell (comprising contacting a cell defective in p53 pathway of a cell (comprising contacting with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting a mammalian cell (comprising contacting the cell with an agent that specifically binds to a HM polypeptide comparising (M3) a p53 pathway of a disease in a patient (comprising: (a) obtaining a biological sample comparisor; (b) contacting the sample with a probe for HM comparisor; (c) comparisor indicates a likelihood disease). (M1) is useful contentifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Comparisors (e.g. cancer). Another two new methods (M2 and contention of the p53 pathway. A probe for HM expression level. Comparisors (e.g. cancer). Another two new methods (M2 and contents) and contents (e.g. cancer). Another two new methods (M2 and contents) are useful for modulating the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring contents. The cell cycle. (M2) and (M3) are useful for modulating the p53 pathway of a cell, thus restoring contents a human p53 pathway modifying protein sequence.
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Best Local S
Matches 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
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10-OCT-2001; 2001US-0328605P.
15-PEB-2002; 2002US-0357253P.
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                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                  LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA
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                                                        VILHTDSRKDSPPAGSPAGRSI YNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                                                                                                                                                                                      MI VFVR FNSSHG FPVEVDSDTS I FQLKEVVAKRQGVPADQLRV I FAGKELRNDWTVQNCD
                                                                                                                                                                                                                                                                                                                               465 AA;
SCWDDVLIPNRMSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCIT
                                 VILHTDSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                                                                                           LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA
                                                                                                                                                                                   MIVFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD
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Pred. No. 2.3e-1
); Mismatches
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                                                                                             New isolated nucleic acid sequence encoding a Parkin polypeptide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in
                                                                                                                                         WPI; 2003-046812/04.
N-PSDB; AAD47680.
                                                                                                                                                                                                                                                                                                                              Cleavage-site
Misc-difference
                                                                Claim 10;
                                                                                                                                                                                                                   29-MAR-2001; 2001DK-00000525.
03-APR-2001; 2001US-0281286P.
                                                                                                                                                                                                                                                  02-APR-2002; 2002WO-DK000221.
                                                                                                                                                                                                                                                                         10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Parkin D126 mutant protein.
                                                                                                                                                                         Jensen
                                                                                                                                                                                               (NSGE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkin
                                                                                                                                                                                               NSGENE
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                                                                                     авваув.
                                                                                                                                                                                                                                                                                                                                                                                                                                      in protein; neurological disorder; apoptosis; gene therapy;
troke; Parkinson's disease; Alzheimer's disease; nootropic;
cerebroprotective; neuroprotective; neurotransplantation;
                                                               71; 71pp; English
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The invention relates to Parkin protein and its corresponding nucleic acid sequence. The nucleic acid sequence is useful for altering the protecolytic processing of Parkin at its potential cleavage site at Asy 126. The invention is used in manufacturing or testing a pharmaceuticity of the invention is used in manufacturing or testing a pharmaceutic.

ye site at Asp pharmaceutical

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RESULT 5
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AC AAY3
XX 21-0
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XX Park
XX Park
XX Pomc
XX Homc
XX Homc
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Best Local Simi
Matches 463;
                            09-FEB-1998;
                                                       09-FEB-1999;
                                                                                                              WO9940191-A1.
 (SHIM/)
                                                                                                                                                                  Parkinson's disease
                                                                                                                                                                                             Human parkin gene
                                                                                                                                                                                                                                                       AAY32502;
                                                                                                                                                                                                                            21-OCT-1999
                                                                                                                                                                                                                                                                                AAY32502 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's disease or ischaemic stroke. It also used for detecting the occurrence of proteolytic processing of Parkin at Asp 126 in a sample, i monitoring a potential disposition for a neurodegenerative disease, and for treating, preventing and/or disgnosing Parkinson's disease or other neurodegenerative disorders. The viral vector is used for transforming neuronal cells in vivo or ex vivo. The invention is useful for neurotransplantation into the CNS of a mammal. It may be used in screening assays to identify compounds that increase or decrease apoptosis. It is also used in gene therapy. The present sequence is huma Parkin mutant protein
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ilarity 99.6%;
Conservative
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                                                     99WO-JP000545
                                                                                                                                                                                           variant protein.
                                                                                                                                                                                                                                                                                protein;
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                                                                                                                                                               gene; parkin
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Pred. No. 2.6e-218;
l; Mismatches 1;
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RESULT 6
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Best Local S
Matches 437
               Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancelung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                                                                            Human
                                                                                                                                                 ABO07157;
                                                                                                                                                                           ABO07157 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is encoded by a gene of the invention, and is implicated the pathology of Parkinson's disease. This sequence is a variant of the parkin gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and investigation of Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 89-94; 114pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene implicated in the pathology of Parkinson's treatment of the disease.
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                                                                                          p53 modifying
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Pred. No. 1.3e-202;
0; Mismatches 0;
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Homo sapiens

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                                                                                                                                                                                                                                                                                                               commodulating agent, by contacting an assay system comprising a purified HM college (human orthologue of genes that modify the p53 pathway in college (human orthologue of genes that modify the p53 pathway in college acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference college are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting and cell (comprising contacting the cell with an agent that specifically binds to a HM polypeptide comprising an HM amino acid comparison contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising; (a) obtaining a biological sample contacting the patient (comparison indicates a likelihood disease). (M1) is useful contentifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Compatition the p53 pathway. A probe for HM expression contents in the p53 pathway. A probe for HM expression contents in the p53 pathway. A probe for modulators of the p53 pathway. A probe for modulators of the p53 pathway. A probe for modulations of the cancer has greater than 25 % expression level. Content the content has greater than 25 % expression level. Content the content was proposed to related to defects in the p53 pathway of a cell thus restoring the p53 pathway of a cell thus restoring content and thorse disease or disease or disease is related to defects in the p63 pathway of a cell thus restoring content points and content through the cell cycle. (M2) and (M3) are content and content of cell proliferation of the cell, so that the cell cycle. (M2) and (M3) are content and content and content and content and content and content and content and content
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10-OCT-2001;
15-FEB-2002;
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                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to identifying (M1) a candidate p53 pathway
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                                                                                                                                                   MIVFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD
        VILHTDSRKDSPAGSPAGKSIYNSPYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP 180
                                                                                                                            MIVFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD
                                                                                                                                                                                                          Conservative
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2001US-0328605P.
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Pred. No. 1.3e
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                    The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25,2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active
                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
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                                                                                                                                                                                                                                                               New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a murine parkin2 polypeptide.
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DB; AAF55258.
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Matches 387
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ntains the mutation Lys161Asn. Mutations
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AAB67532 standard; protein; 464 B

29-MAY-2001 (first entry)

Amino acid sequence of a mutated murine parkin2 polypeptide.

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XX Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral scleros Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic

polynucleotides encoding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
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                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                               sequence contains the mutation Trp4538top. Mutations or deletions in parkin2 gene cause Parkinson's disease in humans. The human parkin2 graits located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multisystem atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, b tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 51-53; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB67533
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a murine parkin2 polypeptide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Мив вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a mutated murine parkin2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOF-)
                                                                                                                                                                          Local
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DB; AAF55260.
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                                                                                                                                                              al Similarity
376; Conserv
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VILHTDSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                            LEQQSIVHIVQRPRRRSHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLA
                                                                 LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA
                                                                                                   MIVEVRENSSYGEPVEVDSDTSILQLKEVVAKRQGVPADQLRVIFAGKELPNHLTVQNCD
                                                                                                                        MIVFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD
                                                                                                                                                                                                                          451
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                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                            80.4%; Score 2087.5; DB 4;
83.2%; Pred. No. 1.2e-174;
tive 29; Mismatches 46;
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                                                                                                                                                                                             451;
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                                                                                                                                                                                                                                                                                                                                                                                                      parkin2 gene
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The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent—biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid
                                                                                                                                                                                                               Example 2; Page 402-403; 678pp; English.
                                                                                                                                                                                                                                                           Identifying modulators of the p53 pathway for use in or cell proliferation disorders, comprises screening modulate activity of a human ortholog of genes that meaning pathway in Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-2002; 2002WO-US017382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiapoptotic; p53 pathway; breast cancer; cytostatic; antiangiogenic; lung cancer; ovarian cancer; anglogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKDCPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCWDDVLÍ PNRWSGECQSPDCPGTRAEFFFKCGAHPTSDKDTSVALNLÍTSNRRSÍPCÍA
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AAB67521
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XX AAB67
AC AAB67
XX 29-MA
CT 29-MA
CX AMino
XX Parki
KW Alzhe
KW Multi

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entry

AAB67521 standard;

protein;

CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV

Amino acid 29-MAY-2001

Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral scle Multi-system atrophy; Wilson's disease; Pick's disease; Prion disea

sequence of a murine truncated parkin2 polypeptide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc sequence, where p53 function is restored), modulating (M3) a p53 pathway c in a mammalian cell (comprising contacting the cell with an agent that c specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample c from the patient; (b) contacting the sample with a probe for HM c expression; (c) comparing the results with a control; and (d) determining the interval of control; and (d) determining c expression indicates a likelihood disease). (M1) is useful c for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 * expression level. C modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell c proliferation disorders (e.g. cancer). Another two new methods (M2 and C M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal c proliferation disorders in the p53 pathway such as angiogenic, c apoptotic or cell proliferation disorders. The present sequence c represents a human n53 nathway modificing norterin
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Best Local Simi
Matches 316;
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                                                                                  GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
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                                                             GPĀFCRĒCKEĀYHEGĒCSAVFEASGTTTQĀYRVDERĀĀĒQĀRWEAASKETIKKTTKPCPR
                                                                                                                                  LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
                                                                                                                                                         LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
                                                                                                                                                                                                      CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                                                                               CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                                                                                                                                                                                                                                     VILHTDSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP 180
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Pred. No. 1.8e-140;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                 -EFFFKCGAHPTSDKETPVALHLIATNSKNITCIT
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Best Local Sin
Matches 307;
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metabolic irregularity.
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                                                                                                                                                                                                                                                                                                                                                     SCWDDVLIPNRMSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCIT 240
                            GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
                                                                                                                                                                                                                                               CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLFCVAGCPNSLIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 40-41; 62pp; English.
GFVFCRDCKEAYHEGDCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPR
                                                                                                        LHHFRILGEEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEQGQRKVTCEGGNGLGC
                                                                                                                                          LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
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                                                                                                                                                                                                                                                                                                                        SCWDDVLIPNRMSGECOSPDCPGTRAEFFFKCGAHPTSDKDTSVALMLITSNRRSIPCIA
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Best Local Simi
Matches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a murine parkin2 polypeptide. The polypucleotide sequence contains a deletion, leading to a truncated protein. Nutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 625.2-27. Parkin2 polypeptides and polypucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a leas active or non-active parkinson reception.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 44-45; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
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                            61 LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA 120
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LEQQSIVHIVQRPRRRSHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLA
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Pred. No. 7.3e-100;
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                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enharyotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL20511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                            New isolated nucleic a
                                                                                                                                                                                                                                                                                           Disclosure; SEQ
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 22134.
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                                               VFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCDLD::|:|:|:|||||::|||
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2000US-00614150
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RESULT 15
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The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral

Claim

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Search completed: February 23, 2005, 13:50:12 Job time : 105.258 secs

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Sequence 6853, Ap
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Patent No. 6716621
Patent No. 6716621
GENERAL INFORMATION:
APPLICANT: Shimizu, No. 6716621uyoshi
APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
FILE REFERENCE: 0652.211000
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 465
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Best Local Similarity
Matches 465; Conserv
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GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
                                                   LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
                                                                                                                     CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLFCVAGCPNSLIKE
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                                LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
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Pred. No. 8.4e-251;
Mismatches 0;
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RESULT 2
US-09-949-016-6516

Sequence 6516, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

NUMBER OF SEQ ID NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 6516

LENGTH: 465

TYPE: PRT

ORGANISM: Human

US-09-949-016-6516
RESULT 3
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08

Sequence 6853, Application US/09949016

Patent No. 6812339

GEMERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION

FILE REFERENCE: CL001307

DETECTION

AND USES THEREOF

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; ORGANISM: Homo
US-09-601-844B-4
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APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's FILE REFERENCE: 0652.2110000
CURRENT APPLICATION NUMBER: US/09/601,844B
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
SOPTWARE: PatentIn version 3.1
SEQ ID NO 4
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GENERAL INFORMATION:
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                                                 CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV 437
                                                                 CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV
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Pred. No. 9.6e-232;
0; Mismatches 0;
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; ORGANISM: Human
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                                                                 ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6854
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-6854
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6854, Applic Patent No. 6812339
GENERAL INFORMATION:
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SEQ ID NO 6853
                                                                                                                NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRETSEQ for Windows
SEQ ID NO 6854
LENGTH: 316
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Best Local 9
Query Match
Best Local Similarity
Matches 316; Conserv
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                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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   Conservative
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               65.4%;
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                 Score 1696.5;
Pred. No. 4.26
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Pred. No. 9.6e-232;
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 Mismatches
                 .2e-161;
                               DB 4;
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   Indela
                                 Length 316;
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RESULT 6
US-09-270-767-32183
US-09-270-767-32183
Sequence 32183, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32183
LENGTH: 117
TYPE: PRT
ORGANISM: Drosophila melanogaster
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Sequence 13, Application US/09914259

Patent No. 6495336

GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
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53.3%; Pred. No. 3.8e-29;
Live 11; Mismatches 40
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GENERAL INFORMATION:

APPLICANT: Chang, Chawnshang

TITLE OF INVENTION. Androgen Receptor Coactivators

FILE REFERENCE: 920920.90011

CURRENT APPLICATION NUMBER: US/09/354,221

CURRENT FILING DATE: 1999-07-15

EARLIER APPLICATION NUMBER: US 60/100,243

EARLIER APPLICATION NUMBER: US 60/100,243

EARLIER FILING DATE: 1998-09-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-354-221-2
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US-09-354-221-2
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Patent No. 6699714
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Best Local Similarity
Matches 72; Conserv
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CURRENT FILING DATE: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                              Ma.
Local 5.
71;
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                                 316 LPVMQBPG-----CTMGICSSCNFÄFCTLCRLTYHGVSPCKVTAEKLMDLRNEYLQADEA 370
                                                                                                                                           289 CVAGCPN-----SLIKELHHFRILGEEQYNRYQQYGAEECVLQMGGVL-CPRPGCG 338
                                                                                                                                                                                                                    232 NSRNITÇ--ITÇTDVRŞPVLVF-QÇNSRHVIÇLDÇFHLYCVTRLNDRQFVHDDQLGYSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 NEFCWVCLGSWEP--HGSSWYN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 LEWCWNCGCEWNRVCMGDHWFD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 -----KKWIKKCDDDSETSNWIAAN------TKECPRCSVTIEKDGGCNHMVCKNQNCK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 ASGTTTQAYRVDERAAEQARWEAASKETIKKTTKECPRCHYPVEKNGGCMHMKCPQPQCR 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 MGGVL---CPRPGCG-AGLLPEPDQRKYTCEGGNGLGCGFAFCRECKEAYHEG-ECSAVFE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 FFKCGAHPTSDKETPVALHLIATNSRNITCITCTDVRSPVLVFQCNSRHVICLDCFHLYC 268
                                                                                                                                                                                                                                                                                           Similarity
                                                                      AGLLPEPDQRKVTCEGGNGLGCGFAFCRECKEAYH-EGECSAVFEASGTTTQAY-----
                                                                                                        CL-NCPEPKCPSVATPGQVKEL----VEAELFARYDRLLLLQSSLDLMADVVYCPRPCCQ 315
                                                                                                                                                                                 NSKLFLCSICFCEKLGSECMYFLEC--RHVYCKACLKDYFEIQIRDGQ------VQ 261
-----RVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQPQCRLE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNQLLRWCESVDCTYAVKVEYABERRVHCK-----CGHVECEACGENWHDEVKCKWL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STK-----IVAEGLĠQTISĊAÄHĠĊ-DILVDDVTVANLVTDARVRVKYQQLITNSFŸ-E
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                                                                                                                                                                                                                                                                8.6%; Score 222; DB 4 ilarity 27.8%; Pred. No. 2e-13; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 240.5; DB 4; Length 27.5%; Pred. No. 3e-15; Vative 42; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                             DB 4; Length 474;
                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                            Indels 60;
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Sequence 15410, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO C

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13
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; ORGANISM: Human
US-09-949-016-10111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-10111
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 CVAGCPN-----SLIKELHHFRILGEEQYNRYQQYGAEECVLQMGGVL-CPRPGCG 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 NSRNITC--ITCTDVRSPVLVF-QCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 8.6%; Score 222; DB 4 1 Similarity 27.8%; Pred. No. 2e-13; 71; Conservative 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                             FCW-----ICMG
                                                                                                                                                                                                                                                                                                                                                                                                    WCWNCGCEWNRVCMG 459
                                                                                                                                                                                                                                                                                                                                                                                                                              NKRLLDQRYGKRVIQKALEEMESKEWLEKNSKSCPCCGTPIEKLDGCNKWTC--TGCMQY 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQPQCRLE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CL-NCPEPKCPSVATPGQVKEL----VEAELFARYDRLLLQSSLDLMADVVYCFRFCCQ 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 2, Application US/08398008A
Patent No. 5665588
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Best Local :
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SEQ ID NO 15410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/126,501
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Dr. Benjamin Aaron
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5705CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA Encu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 506
                                                                                                                                                                                                                   OPERATING SYSTEM: Macintosh SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/398,008A FILING DATE: March 2, 1995
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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nes 79; Conserv
                                TELEPAX:
                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 LHLIATNSRNITCITCTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 CSTCRQATLTLTQGPSCWDDVLIPNRMSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMKC--SLCKTDFCFNCGSK----IGNNHDHFVD 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMKCPQPQCRLEWCWNCGCEWNRVCMG---DHWFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPSI---PLAMLTKILKSPSLVDRYYNLFKKSQYEWIGNLLPNRLVKCPRVGCDEVIPR 345
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                                                                                                                                                                                                                                                                                                                                                                                                  Texas
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8011 Candle Lane
                                  (713) 777-6908
                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                           PE: Diskette, 3.5 inch, MACINTOSH IIci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    & Adler, P.C
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                                                                                                                                                                                                                                                                                                                               1.44 Mb storage
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                                                                                                                                                                                                                            ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Amino acid sequence of Natural Killer Lytic
OTHER INFORMATION: Associated Protein encoded by nucleotides
OTHER INFORMATION: 190 to 1953 of Sequence ID. No. 5981705 1
Patent No. 5981705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08893333A Patent No. 5981705
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 17
SEQ ID NO 2
                                                                                                                                         Matches
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kornbluth, Jacki
TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated Protein
FILE REFERENCE: DS705CIP/D
CURRENT APPLICATION NUMBER: US/08/893,333A
CURRENT FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                                                                    LENGTH: 587
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: P:
HYPOTHETICAL: NO
ANTI-SENSE: NO
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   118
                                 178 QGPSCWDDVLIPNRMSGECQSPHCPGTSAEF-FFKCGAHPTSDKETPVALHLIATNSRNI 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPGCGAGLL-----PEPDQRKVTCEGGNGLGCGFAFCRECKEAYHEGECSAVFEASGT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCITC----TDVRSPVLVFQCNSRHVICLDCFHLY------CVTRLND-- 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGPP-----PEALPAE-----PAAEAEAAAAAGAEPGFDDEE--AAEGGGPGGEEV
ECPLCLVRLPPERAPRLL---SCPHRSCRDCLRHYLRLEISESRVPISCPECSERLNPHD 174
                                                                     QGPP-----PEALPAE-----PAAEAEAAAAAGAEPGFDDEE--AAEGGGPGGEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCWLCMKEISDLHYLSPSGCTFWGKKPWSR 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAQTLRVRTKHTSGLSY----GQESGPDDIKPCPRCSAYIIKMNDGSCNHMTC--AVCGCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECPLCLVRLPPERAPRIL---SCPHRSCRDCLRHYLRLEISESRVPISCPECSERLNPHD 174
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                                                                                                                                                        24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4%; Score 167; DB 1; 24.2%; Pred. No. 8.4e-08;
                                                                                                                                       Score 167; DB 2; L; Pred. No. 8.4e-08; 24; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GC-----EWNR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 587;
                                                                                                                                                                        Length 587;
                                                                                                                                         Indels 112;
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US-09-248-796A-16471
US-09-248-796A-16471
; Sequence 16471, Application US/09248796A
; Patent No. 6747137
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US-09-538-092-598
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SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 598
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Best Local Similarity 21.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YML068W
-09-538-092-598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
CURRENT FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (0) ... (0)
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ORGANISM: Saccharomyces
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 464
                                                                                                        400
                                                                                                                                                           342 VSLŠTDIIEEYLDDTVTSYERKRKLEAKYGRRVLELEVNDYLÄEKMLDLÄIKKE--GSNL 399
                                                                                                                                                                                                       381 FEASGTTTQAY-----
                                                                                                                                                                                                                              289 YCPYACVTCRR--CDSWCTKEDLDDAMIQCQ----KCHFVFCFDCLHAWHGYNNKCGKK 341
                                                                                                                                                                                                                                                                                                 237 LKLEDFKSYKKMLKALFTÞLI---ÞVSFLKE----VIDTELCERYEKMFYNQAATRLSK 288
                                                                                                                                                                                                                                                                                                                                                                      177 NYHCCICMEMEKGVRMIKLPCENANVEHYLCRGCAKSYFTAMIQENRISSVRCPQCEYKE
                                                                                                                                                                                                                                                                                                                                                                                                      235 NITCITCTDVRSPYLVFQ-----CNSRHVICLDCFHLYCVTRLNDRQF--YHDPQLGYS- 286
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                                                                                           QRCPKCKVVVERSEGCNKMKC--EVCGTLFCFICG 432
                                                                                                                           KPCPRCHYPYEKNGGCWHMKCPQPQCRLEWCWNCG 450
                                                                                                                                                                                                                                                               -----VLCPRPGCGAGLLPEP-DQRKVTCEGGNGLGCGFAFCRECKEAYH--EGECSAV 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149; DB 4;
Pred. No. 3.8e-06;
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RESULT 15
US-08-854-764-2
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                                TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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LENGTH: 328
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APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER: OF SEO ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                    NAME: Savereide, Paul B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                 APPLICATION NUMBER: 08/286,530 FILLING DATE: 05-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            FILING DATE: 12-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Innes, Michael
APPLICANT: Creasey, Abla
TITLE OF INVENTION: Production of
TITLE OF INVENTION: Inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 450.
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 IGCSEHHEFCFNCKXENHL-PCPC------WVSKRWIKKCNDDSETAHWIDANT 104
amino acid
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              352 amino acids
                                                                          : 510-601-2585
510-655-3542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiron Corporation
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30.2%; Pred. No. 1.4e-05;
tive 15; Mismatches 37;
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Search completed: February 23, 2005, 14:01:03 Job time : 27.8801 secs
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Best Local Similarity 18.3%; Pred. No. 0.0001;
Matches 70; Conservative 56; Mismatches 116; Indels 140; Gaps 16;
                                                                302 ENNFTSKQECLRACKKGFIQRI 323
                                                                                                                              247 PVLVFQCNSRHVICLDCFH--LYCVT-----RLNDRQFVHDPQLGYSLP----- 288
                                                                                                                                                                                                198 CERFKYGGCLGNMNNFETLEECKNICEDGPNGFQVDNYGTQLNAVNN----SLTPQSTKV 253
                                                                                                                                                                                                                                 212 -----CGAHPTSDKETPVALHLIATNSRUITCITCTDVRS 246
                                                                                                                                                                                                                                                                  156 NANRI-----IKTTLQQEKPDFCFLE-----EDPGICRGY!TRYFYNNQTKQ 197
                                                                                                                                                                                                                                                                                                 158 QPGKLRVQCSTCRQATLTLTQGPSCWDDVLIPNRMSGECQSPH-CPGTSAEFFFK----- 211
                                                                                                                                                                                                                                                                                                                                                                  121 VILHT--DSRKDSPPAGSPAGRSIYNSF-----YVY------CKGPCQRV 157
                                                                                                 289 ------CVAGCPNSLIKEL 301
                                                                                                                                                                                                                                                                                                                                    98 --MHSFCAFKADDGPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRFESLEECKKMCTRD 155
                                                                                                                                                                                                                                                                                                                                                                                                      61 IQKESTLHLVLR------LRGGDSEE------DEEHTIITDTELPFLKL------ 97
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Regult
No.
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Maximum Match 100%
Listing first 45 summaries
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544.5
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10N_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10N_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10N_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10N_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10N_PUB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US10N_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                 Length
      GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                 DB
16 US-10-473-226-2
16 US-10-776-604-2
17 US-10-839-26-4
18 US-10-473-226-4
19 US-10-776-604-4
19 US-09-785-548-4
14 US-10-239-249-2
15 US-10-313-203-10
15 US-10-313-203-17
19 US-09-864-761-36750
10 US-10-425-114-55407
15 US-10-425-114-55407
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  Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
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Sequence 2, Appli
Sequence 10, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 179787,
Sequence 55407, A
Sequence 53407, A
Sequence 13, Appl
                                                                                                                                                                                                                                                                                 Description
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e 40231,	equence 21259	equence 547	e 15	e 18465	e 1	e 56467	e 1687	e 562	equence 1113	equence 2652	equence 3	equence 56,	e 854,	21779	Sequence 133385,	140793	1727, A	e 39657	38443,	Sequence 148905,	18,	e 2, Appl	e 182	44	0	57	N	Sequence 42, Appl	equence 63	e 14767	Sequence 102, App

ALIGNMENTS

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; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: mat_peptide
; LOCATION: (1):.()
; OTHER INFORMATION: Native Parkin
US-10-473-226-2
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                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 2
; LENGTH: 46
; TYPE: PRT
                                                                                                                                                              Matches
                                                                                                                                                                                   Query Match
Best Local Similarity
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TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin FILE REFERENCE: 506-204-WO CURRENT APPLICATION NUMBER: US/10/473,226
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: DK PA 2001 00525
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/281,286 PRIOR FILING DATE: 2001-04-03
                                                                                                                                                         tch 100.0%; Score 2596; DB 16; Length sal Similarity 100.0%; Pred. No. 2.2e-220; 465; Conservative 0; Mismatches 0; Indels
61 LDQQSIVHIVQRPWRKGQEMMATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                  465
                                                                                                 MIVFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD
                                                                    MIVFVRFNSSHGFPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD
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APPLICANT: Mizuno, Yoshikuni
APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: DNAs or Genes Participating in
FILE REFERENCE: 0652.2110001
CURRENT APPLICATION NUMBER: US/10/776,604
CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 09/601,844
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: JP 10/27531
PRIOR APPLICATION NUMBER: JP 10/27531
PRIOR FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
TENGTH: 465
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
-10-776-604-2
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                                                    SCWDDVLIPNRMSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCIT
                                                                                               VILHTDŚRKDŚPPAGŚPAGRŚIYNŚPYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                                                                                                    VILHTDSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                                                                                                                                                                     LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA 120
CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
                                 SCWDDVLIPNRMSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCIT
                                                                                                                                                                  LDQQSIVHIVQRPWRKGQEWNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKDCPR
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APPLICANT: FATTER, MATTHEW J.

FITILE OF INVENTION: PARKINSON'S DISEASE MARK
FILE REFERENCE: 07039-448001

CURRENT APPLICATION UNMBER: US/10/839,688

CURRENT FILING DATE: 2004-05-05

PRIOR APPLICATION NUMBER: US 60/468,832

PRIOR FILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 81

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 9

SEQ ID NO 9

SEQ ID NO 9

CREANISM: 465

TYPE: PRT
ORGANISM: Homo Sapiens
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Matches 4
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465; Conservative
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                                                                         GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKDCPR 420
                 CHYPYEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV
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CHVPVEKNGGCMIMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV
                                                         GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKET1KKTTKPCPR
                                                                                                                   LHHFRILGEBÓYNRYQQYGABECVLOMGGVLCPRÞGCGAGLLÞEÞÐQRKVTCEGGNGLGC
                                                                                                                                    LHHFRILGEBQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC 360
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Sequence 4, Application US/10473226

publication No. US20040198650A1

GENERAL INFORMATION:
APPLICANT: NEGENEAL/S

ITILE OF INVENTION: Means for inhibiting proteolytical profile REFERENCE: 506-204-WO
CURRENT APPLICATION NUMBER: US/10/473,226

CURRENT FILING DATE: 2003-09-29

PRIOR APPLICATION NUMBER: DK PA 2001 00525

PRIOR APPLICATION NUMBER: US 60/281,286

PRIOR APPLICATION NUMBER: US 60/281,286

PRIOR FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 7

FORWANDE: DATE: 2001-04-03
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US-10-776-604-4
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Sequence 4, Application US/10776604
Publication No. US20050003385A1
GEMERAL INFORMATION:
APPLICANT: Shimizu, Nobuyoshi
APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: DNAs or Genes Participating
FILE REFERENCE: 0652.2110001
CURRENT APPLICATION NUMBER: US/10/776,604
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SEQ ID NO 4
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Best Local Similarity
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NAME/KEY: mat peptide
LOCATION: (1)...()
OTHER INFORMATION: Parkin with a D126E mutation
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2.5e
1; Mismatches
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Sequence 4, Application US/0978548
; Patent No. US20020155577A1
; GENERAL INFORMATION: PHARMACEUTICALS, INC.
; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE FILE REFERENCE: ST00005
; CURRENT APPLICATION NUMBER: US/09/785,548
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; SEQ ID NO 4
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-548-4
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US-09-785-548-4
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 437
 Query Match
Best Local Similarity
Matches 155; Conserv
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Best Local Similarity
Matches 437; Conserv
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PRIOR APPLICATION NUMBER: 09/601,844
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR RILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: JP 10/27531
PRIOR FILING DATE: 1998-02-09
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
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 33.5%;
ilarity 99.4%;
Conservative
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Score 870; DB 9;
Pred. No. 1.3e-68;
0; Mismatches 1
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Pred. No. 1.5e-203;
0; Mismatches 0;
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                                   Length 156;
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APPLICANT: HONER, MARIUS

APPLICANT: LINK, WOLFGANG

APPLICANT: BAUMEISTER, RALF

TITLE OF INVENTION: NEMATODES AS MODEL ORGANISMS FOR INVESTIGATING

TITLE OF INVENTION: NEMATODES AS MODEL ORGANISMS FOR FINDING STEATANCES AND

TITLE OF INVENTION: DISEASE, USES AND METHODS FOR FINDING SUBSTANCES AND

TITLE OF INVENTION: GENES WHICH CAN BE USED IN TRATTING SUCH DISEASES, AND

TITLE OF INVENTION: IDENTIFICATION OF A NEMATODE GENE

TITLE OF INVENTION: IDENTIFICATION OF A NEMATODE GENE

TITLE OF INVENTION: USERS: US/10/239,249

CURRENT APPLICATION NUMBER: US/10/239,249

CURRENT APPLICATION NUMBER: PCT/EP01/03214

PRIOR APPLICATION NUMBER: DO3-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PATCHININ Ver. 2.1

SOFTWARE: PATCHININ VER. 2.1
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US-10-239-249-2
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LENGTH: 386
TYPE: PRT
ORGANISM: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
        323
                                   378 SAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCP 437
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                                                                                                                EECV-LQMGGVLCPRPGCGAGILLPEP--DQRKVTCEGGNGLGCGFAFCRECKEAYHEGEC 377
                                                                                                                                                                                                     DCFHLYCVTRLNDRQFVHDPQLGYSLPC-VAGCPNSLIKELHHFRILGEEQYNRYQQYGA 320
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    VCQSEDDLTRT-
                                                                                                                                                              FCFRDYLLSQLERFGFVNQPPHGFTIFCPYPGC-NRVVQDVHHFHIMGQTSYSEYQRKAT 271
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TIDATTRRCPKCHVATERNGGCAHIHC-
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APPLICANT: Gu, Wei
APPLICANT: Nikolaev, Anatoly
TITLE OF INVENTION: P53-ASSOCIATED PARKIN-LIKE CY:
TITLE OF INVENTION: AND METHODS
FILE REFERENCE: 68106
CURRENT APPLICATION NUMBER: US/10/313,203
CURRENT FILIN DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 56
TYPE: PRT
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; Publication No. US20040029134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; APPLICANT: Nikolaev, Anatoly
; TITLE OF INVENTION: P53-ASSOCIATED PARKIN-LIKE CY;
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 68106
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
RESULT 10
US-09-864-761-36750
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US-10-313-203-17
; Sequence 17, Application US/10313203
; Publication No. US20040029134A1
; GENERAL INFORMATION:
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US-10-313-203-10
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Best Local (
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                                                                         238 CITCTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGC 293
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                                                         1 CITCTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGC
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100.0%; Pr
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Pred. No. 6.7e-21;
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                                                                                                                        Mismatches
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Sequence 36750, Application US/09864761 Patent No. US20020048763A1

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PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-08-03

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

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PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                            Local Similarity
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
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FILING DATE: 2001-01-30
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R INFORMATION:
R INFORMATION:
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APPLICATION NUMBER: PCT/US01/00661
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Rank, David R.
                                           YNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNG 357
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                                                                                                                10.1%; Score 263; DB 9; Length 46; ilarity 100.0%; Pred. No. 1e-15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             NN: MAP TO AL035697.18

NN: EXPRESSED IN PLACENTA, SIGNAL = 0.68

NN: EXPRESSED IN LUNG, SIGNAL = 0.94

NN: EXPRESSED IN HELA, SIGNAL = 0.94

NN: EXPRESSED IN BT474, SIGNAL = 0.63

NN: EXPRESSED IN BT474, SIGNAL = 0.68

NN: EXPRESSED IN BARIN, SIGNAL = 0.68

NN: EXPRESSED IN BONE MARROW, SIGNAL = 0.77

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96

NN: EXPRESSED IN BONE MARROW SIGNAL = 0.96

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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Plant Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 55407
LENGTH: 604
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 199787
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Best Local Similarity
Matches 71; Conserv
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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ORGANISM: Oryza sativa
FEATURE:
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3051-106-A7_FLI.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 NRRRLTCAICFDVFDTGGMRSAGCSHFYCVSCWRGYV-----RAAVGDGARCLSLRCPD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 NSRNITCITCTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCV-
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Barbazuk, Brad
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RESULT 14
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US-10-080-608A-13
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 503
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Best Local Similarity
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/080,608A CURRENT FILING DATE: 2002-02-21
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ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                         164 STK-----IVAEGLGQTISCAAHGC-DILVDDVTVANLVTDARVRVKYQQLITNSFV-E 215
                                                                                                                                                                                                                                                                                                                                      269
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9.3%; Score 242.5; DB 15; Length 604;
Similarity 27.7%; Pred. No. 1.7e-12;
70; Conservative 31; Mismatches 97; Indels 55;
                                                       NEFCWVCLGSWEP--HGSSWYN 335
                                                                                             LEWCWNCGCEWNRVCMGDHWFD 464
                                                                                                                                                                                                                                                                                                                            VTRLNDRQFVHDPQLGYSLPCVA-GCPNSLIKELHHFRILGEEQYN-RYQQYGAEECVLQ 326
                                                                                                                                                                                                                                                                                                                                                                     FFKC-AHVINPFNATEAIKQKTSRSQCEECEICFSQLPPDSMAGLECGHRFCMPCWHEYL
                                                                                                                                                                     ASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQPQCR 442
                                                                                                                                                                                                                  CNOLLRWCPSVDCTYAVKVPYAEPRRVHCK----
                                                                                                                                    ----KKWIKKCDDDSETSNWIAAN-
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                                                                                                                                  TKECPRCSVTIEKDGGCNHMVCKNQNCK 315
                                                                                                                                                                                                            -- CGHVFCFACGENWHDPVKCRWL--
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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Edward
TITLE OF INVENTION: Nanostructures Containing PNA Joining and Func
FILE REFERENCE: NANF.P-004
CURRENT APPLICATION NUMBER: US/10/370,685
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/080,608
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 159
SOPTWARE: PatentIn version 3.2
SEQ ID NO 102
TENCTH: 503
                                                                                  ; OTHER INFORMATION: Clone ID: US-10-424-599-147673
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US-10-424-599-147673
US-10-424-599-147673, Application US/10424599
Publication No. US20040031072A1
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                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FULE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 147673
LENGTH: 585
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/10370685 Publication No. US20030215903A1 GENERAL INFORMATION:
                                                                                                                                                           NAME/KEY: unsure LOCATION: (1)..(585) OTHER INFORMATION: v FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.3%; Score 240.5; DB 15; Best Local Similarity 27.5%; Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 MGGVL--CPRPGCG-AGLLPEPDQRKVTCEGGNGLGCGFAFCRECKEAYHEG-ECSAVFE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 STK-----IVAEGLGQTISCAAHGC-DILVDDVTVANLVTDARVRVKÝQQLITNSFV-E 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 VTRLNDRQFVHDPQLGYSLPCVA-GCPNSLIKELHHFRILGEEQYN-RYQQYGAEECVLQ 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 FFKC-AHVINPFNATEAIKOKTSRSOCEECEICFSOLPPDSMAGLECGHRFCMPCWHEYL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 FEKCGAHPTSDKETEVALHLIATNSRNITCITCTDVRSPVLVFQCNSRHVICLDCFHLYC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEFCWVCLGSWEP--HGSSWYN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEWCWNCGCEWNRVCMGDHWFD 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNQLLRWCPSVDCTYAVKVPYAEPRRVHCK-----CGHVFCFACGENWHDPVKCRWL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----KKWIKKCDDDSETSNWIAAN-----
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                                                                                                                                                                                                                                                 (585)
                                                                                                                                                                                                      unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Mismatches 111; Indels 37;
                                                                                                           PAT_MRT3847_10436C.1.pep
Score 233.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKECPRCSVTIEKDGGCNHMVCKNQNCK 315
DB 15;
Length
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Search completed: February 23, 2005, 14:33:24 Job time : 75.0113 secs

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Scoring table: Title: Perfect score: OM protein - protein search, using sw model Total number of hits satisfying chosen parameters: Searched: Run on: BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-622-817-8 2596 1 MIVFVRFNSSHGFPVEVDSD......CWNCGCEWNRVCMGDHWFDV 465 283416 Begs, 96216763 residues February 23, 2005, 13:34:50 ; Search time 19.3575 Seconds (without alignments) 2311.294 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	₅	4	ω	2	_	Result
142.5	143.5	•	149	152.5	155	157	158.5	159	162.5	173	174	174.5	178.5	178.5	180.5	182.5	186.5	188	190.5	193	195	196.5	198.5	205	205	219.5	220	490	Score
5.5	5.5	5.7	•	٠	6.0	6.0	٠	6.1	6.3	6.7	6.7	6.7	6.9	6.9	7.0	7.0	7.2	7.2	7.3	7.4	7.5	7.6	7.6	7.9	7.9	8.5	8.5	18.9	atch
155	155	1209	464	816	532	488	451	518	498	565	348	408	688	497	594	551	324	1048	436	542	320	514	644	491	437	1753	543	357	Length
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	ຎ	ນ	N	N	DB
JH0226	JH0227	T52523	S48329	T25555	T04748	T29562	T16481	E84536	JC5983	F84721	T47494	T47498	B86448	G87793	T04783	S38086	T16983	T31653	H87793	A84725	T45909	G84724	T02366	F87793	T16477	T00350	H84724	T23460	
ubiquitin / riboso	ubiquitin / riboso	hypothetical prote	ы					hypothetical prote	protein kinase C-i	0			hypothetical prote	'n	•			hypothetical prote	protein C27A12.8 [_	hypothetical prote		hypothetical prote	'n	•	hypothetical prote		1 prot	Description

ALIGNMENTS

Db Qy	Оу	D 69	B &	D 29	B &	D Q	Query M Best Lo Matches	RESULT 1 T23460 T23460 T23460 C;Species: C;Date: 15- C;Accession R;McMurray, submitted t A;Reference A;Accession A;Status: p A;Molecule A;Residues: A;Cross-ref A;Experimen C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics:
379 AVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQ 438	322 ECV-LQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGCGFAFCRECKEAYHEGECS 378 : :	262 DCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKELHHPRILGEEQYNRYQQYGAE 321 :	202 PGTSABEFFKCGAHPTSDKETÞVALHLIATNSRNITCITCTDVRSPVLVFQCNSRHVICL 261 ; ; ; ;	142 IYNSFYYYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGPSCWDDVLIDNRMSGECQSPHC 201	82 ATGGDDPRNAAGGCEREPQSLTRVDL8SSVLPGDSVGLAVILHTDSRKDSPPAGSPAGRS 141	22 SIFQLKEVVAKROGVPADQLRVIFAGKELRNDWTVQNCDLDQQSIVHIVQRPWRKGQEMN 81	Query Match 18.9%; Score 490; DB 2; Length 357; Best Local Similarity 26.7%; Pred. No. 1.8e-29; Matches 119; Conservative 53; Mismatches 154; Indels 120; Gaps 12;	RESULT 1 T23460 T23460 T23460 C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T23460 C;Accession: T23460 C;Accession: T23460 C;Accession: T23460 A;McTence number: Z19743 A;Accession: T23460 A;Reference number: Z19743 A;Accession: T23460 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;McCession: T23460 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Gcatus: preliminary; translated from GB/EMBL/DDBJ A;Gcatus: preliminary; translated from GB/EMBL/DDBJ A;Ccatus: preliminary; translated from GB/EMBL/DDBJ A;Ccatus: preliminary; translated from GB/EMBL/DDBJ A;Ccatus: preliminary; translated from GB/EMBL/DDBJ A;Caendius: 1.357 <wil- 1;="" 218="" 286="" 2;="" 2<="" 311="" 33="" 3;="" 72="" a;caendius:="" a;cxperimental="" c;genetics:="" clone="" k08e3="" source:="" td=""></wil->

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233

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В
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A;Molecule type: mRNA
A;Residues: 1-1753 <15H>
A;Cross-references: UNIPROT:Q8IWT3; EMBL;AB014608; NID:g3327229; PIDN:BAA31683.1;
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                          R;IShikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. DNA Res. 5, 169-176, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete A;Reference number: Z14142; MUID:98403880; PMID:9734811
                                                                                                                                                                                                 A;Note:
                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein KIAA0708 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00350
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A:Map position: 2
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A;Molecule type: DNA
A;Residues: 1-543 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: H84724
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9SKC3; GB:AE002093; NID:g4887759; PIDN:AAD32295.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ARI-like RING zinc finger protein [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Best Local
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les 125; Conser
                                                                                                                                                                                              KIAA0708
                                                       1012
                                                                        1 MIVFVRFNSSHGFPVEV---DSDTS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 VAGCENSLIKELHHFRILGEEQYNRY--QQYGAEECVLQMGGVLÇPRPGÇGAGLL---PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 NIOCGICFESYTREEIARVSCGHPYCKTCWAGYITTKIEDGFGCLRVKCPEPS-----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 NITCITCTDVRSEVLVEQCNSRHVICLDCEHLYCVTRLND-----RQEVHDPQLGYSLEÇ 289
                            MWLLLKFNQTEEVSVETLLKDSDLSPELLLQALVPLTSGNGPLTLHBGQDFPHGGVLRLH 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----BAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQPQCRLEWCWNC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSYDVSCL-----CSYRFCWNCSEDAHSPVDCDTV-
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                                                                                                                     Conservative
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                                                                                                                               8.5%;
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25.9%;
                                                                                                                  57;
                                                                                                          Score 219.5; DB 2;
Pred. No. 2.2e-08;
7; Mismatches 181;
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Pred. No. 5.9e-09;
3; Mismatches 83
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                                                                                                        Indels
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A;Introns: 41/3; 134/3; 185/3; 223/3; 254/2; 287/2; 414/3
                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:F56D2.5
                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q20871; EMBL:U13644; NID:g532100; PID:g1945502; PIDN:AAB5268:
A;Experimental source: strain Bristol N2; clone F56D2
                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-437 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16477
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z18519
A; Accession: T16477
                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, August 1994
A;Description: The sequence of C. elegans cosmid F56D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F56D2.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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Best Local
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136 SPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGPSCWDDVLIPNRMSGE 195
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                                                                                                                                        18 DSDTSIFQLKEVVAKRQGVPADQLRVIFAGKEL--RNDWTVQNCDLDQQSIVHIVQRPWR 75
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                                                                                   KGQEMNATGGDDFRNAAGGCEREFQSLTRVDLSSSVLFGDSVGLAVILHTDSRKDSPFAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEKALLRGY-VESC---SNLTWCTNPQGCD-----RILCRQGLGCGTTCSKCGWA 1423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRRDDRÞQILMYAÁÞEÞMGÞCRGQADVÞFĊGSQSETSKÞSÞEAV-----ÁŤLASLQLÞ 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------AGRIMSPQ----EVEGLMKQTVRQVQETLNLEPDVAQHLLAHSHWGAE 1272
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                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCLVLBAWOKGPNPPGTLG---HTVAGGV-----ACTSTDVLSCIL--HLLGQGYV---- 1175
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                                                   -GFDNLYDPTVTIEGTSDSGDQFHLPLDILP-----PIRLKFHLPNDYPTVS 88
                                                                                                                                                                                                                  7.9%; Score 205; DB 2; 20.2%; Pred. No. 6.3e-08;
                                                                                                                                                                                                   66; Mismatches
                                                                                                                     ----BALESVLREKKLAKSSDWSDKNAEI--QGIIEV-----
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Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: geneseqp1980s:*
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Copyright (c) 1993 - 2005 Compugen
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236	236.5	236.5	236.5	236.5	236.5	239	240	240.5	240.5	251	251	251	252	263	263	263	263	263	263
9.1	9.1	9.1	9.1	9.1	9.1			9.3	9.3	9.7	9.7	9.7	9.7	10.1	10.1	10.1	10.1	10.1	10.1
53	557	557	445	445	445	520	511	503	503	105	105	63	106	46	46	46	46	46	46
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Aab67528 Amino aci	Adq96028 T cell ac	Aay98059 Human Rin	Adq96026 T cell ac	Adq96154 T cell ac	Aab21034 Human nuc	Adp22562 Sea-squir	Abb63665 Drosophil		Abb61708 Drosophil	Adm96487 Modified	Aab67520 Amino aci	Aab67522 Amino aci	Adm96489 Modified	Abg38830 Human pep	Abg50898 Human liv	Aam56839 Human bra	Aam69222 Human bon	Abb21452 Protein #	Abb30873 Peptide #

ALIGNMENTS

AAY32501;

AAY32501 standard; protein;

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RESULT 1
AAV32501
ID AAV3
XX AAV3
AC AAY3
XX PAIK
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DE Huma
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PF 09-F
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                                                                                                                                                                                                                                                                   This sequence is encoded by a gene of the invention, and is implicated in the pathology of Parkinson's disease. This sequence is a variant of the parkin gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and
                                                                                                                                                         Sequence 465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 83-88; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene implicated in the pathology of Parkinson's treatment of the disease.
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                                       New isolated nucleic acid sequence encoding a Parkin polypeptide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in
                                                                                                                                                      WPI; 2003-046812/04.
N-PSDB; AAD47679.
                                                                                                                                                                                                                                                                                                                 29-MAR-2001; 2001DK-00000525.
03-APR-2001; 2001US-0281286P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Parkin protein; neurological disorder; apoptosis; gene therapy; ischaemic stroke; Parkinson's disease; Alzheimer's disease; nootropic; transgenic; cerebroprotective; neuroprotective; neurotransplantation.
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Claim 10; Page 69;

71pp; English

Homo sapiens

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Matches 4
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                          Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancellung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                                                                                                 Human
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10-OCT-2001;
15-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                    Sequence
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2001US-0328605P
2002US-0357253P
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                                                                                                                                                                                                                                                                          Score 2596; DB 6;
Pred. No. 2.3e-219;
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                                                                                           New isolated nucleic acid sequence encoding a Parkin polypeptide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in
                                                                                                                                                                       Jensen
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03-APR-2001;
                                                                                                                                                                                                                                                                                                                            Cleavage-site
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                  screening
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DB; AAD47680.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    rkin protein; neurological disorder; apoptosis; gene therapy;
stroke; Parkinson's disease; Alzheimer's disease; nootropic;
c; cerebroprotective; neuroprotective; neurotransplantation;
                                                                                  assays.
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2001US-0281286P.
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The invention relates to Parkin protein and its corresponding nucleic acid sequence. The nucleic acid sequence is useful for altering the proteolytic processing of Parkin at its potential cleavage site at Asp 126. The invention is used in manufacturing or testing a pharmaceutical composition for treating and/or preventing a neurological disorder, e.g.

Claim 10;

Page 71; 71pp;

English.

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Best Local Similarity
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(SHIM/) SHIMIZU
                                            09-FEB-1999;
                                                                                             WO9940191-A1.
                                                                       12-AUG-1999.
                                                                                                                                         Parkinson's disease related
                                                                                                                                                                                          21-OCT-1999
                                                                                                                                                                                                                                        AAY32502 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's disease or ischaemic stroke. It also used for detecting the occurrence of proteolytic processing of Parkin at Asp 126 in a sample, in for treating, preventing and/or disgnosing Parkinson's disease, and neurodegenerative disorders. The viral vector is used for transforming neurodegenerative disorders. The viral vector is used for transforming neuronal cells in vivo or ex vivo. The invention is useful for neurotransplantation into the CNS of a mammal. It may be used in apoptosis. It is also used in gene therapy. The present sequence is huma Parkin mutant protein
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                                                                                                                                                              variant protein.
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                                                                                                                                        gene;
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Pred. No. 2.6e-218;
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Best Local :
                         Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cance lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                       AB007157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is encoded by a gene of the invention, and is implicated the pathology of Parkinson's disease. This sequence is a variant of the parkin gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and investigation of Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 437 AA;
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                                                                                                                                                                                                                                                                                                                                CC modulating agent, by contacting an assay system comprising a purified HM CC polypeptide (human orthologue of genes that modify the p53 pathway in CC brosophila) or nucleic acid with a test agent under conditions, where but CC for the presence of the test agent, the system provides a reference CC activity, and detecting a test agent-biased activity of the assay system. CC also included are modulating (M2) a p53 pathway of a cell (comprising CC contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid CC sequence, where p53 function is restored), modulating (M1) a p53 pathway CC in a mammalian cell (comprising contacting the cell with an agent that CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: a) obtaining a biological sample CC from the patient; (b) contacting the sample with a probe for HM corporation; (c) comparing the results with a control; and (d) determining CC whether the comparison indicates a likelihood disease). (M1) is useful CC whether the comparison breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. CC Modulators identified by (M1) are useful in a variety of diagnostic and CC to defects in the p53 pathway. A probe for HM expression CC contaction of the cell, so that the cell undergoes normal CC proliferation of spotters (e.g. cancer). Another two new methods (M2 and CC M3) are useful for modulating the p53 pathway of a cell, thus restoring CC proliferation or progression through the cell cycle. (M2) and (M3) are calculating defects in the p53 pathway such as angiogenic, CC apoptetic or cell proliferation disorders. The present sequence
                                                                                                                                                                                                                 Matches 437;
                                                                                                                                                                                                                               Query Match
Best Local
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10-OCT-2001;
15-FEB-2002;
                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
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2001US-0328605P.
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                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17-19; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB67517
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The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's di

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolic irregularity.
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                       CHVPVEKNGGCM::MKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV
CNVPIEKNGGCMHMKCPQPQCKLEWCWNCGCEWNRACMGDHWFDV
                                                                                     GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKDCPR
                                                                                                                                LHHFRILGEEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEQGQRKVTCEGGNGLGC
                                                                                                                                                        LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCBGGNGLGC
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                                                               GPVFCRDCKEAYHEGDCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPR
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RESULT 9
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XC AAB6
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DE Amin
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KW Park
KW Malzh
KW Mult
KW braik
KW meta
      Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral scle: Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
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Best Local Similarity 83.2
Matches 387; Conservative
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CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV 465
                                                  GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
                                                                                                                LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQ;RKVTCEGGNGLGC
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                            GFVFCRDCKEAYHEGDCDSLLEPSGATSQAYRVDKRAAEQARWEEA; KETIKKTNKPCPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a mutated murine parkin2 polypeptide
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VILHTDSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                                                                                                                                  LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA 120
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83.2%; Pred. No. 1.2e-174;
tive 29; Mismatches 46;
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The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent, the system provides a resay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying modulators of the p53 pathway for use in or cell proliferation disorders, comprises screening modulate activity of a human ortholog of genes that metallic activity of a human ortholog of genes that metallic activity of a human ortholog of genes that metallic activity of a human ortholog of genes that metallic activity of a human ortholog of genes that metallic activities are not seen that metallic activities are not seen as a seen activities and the seen activities are not seen as a seen activities and the seen activities are not seen as a seen activities are not seen as a seen activities are not seen as a seen activities are not seen as a seen activities are not seen as a seen activities and the seen activities are not seen as a seen activities are not seen as a seen activities are not seen as a seen activities are not seen as a seen activities are not seen as a seen activities are not seen as a seen activities and the seen activities are not seen activities and the seen activities are not seen as a seen activities are not seen as a seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities and the seen activities are not seen activities activities and the seen activities are not seen activiti
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10-OCT-2001; 2001US-0328605F
15-FEB-2002; 2002US-0357253P
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RESULT 12
AAB67521
ID AAB67
XX AAB67
AC AAB67
XX 29-MA
DT 29-MA
XX XX
DE Amino
XX Parki
KW Parki
KW Alzhe
KW Multi

AAB67521 standard;

protein;

Amino 29-MAY-2001

acid

sequence

of a murine truncated parkin2 polypeptide

(first

entry)

Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral scle Multi-system atrophy; Wilson's disease; Pick's disease; Prion disea

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CC Modulators identified by (M1) are useful in a variety of diagnostic and CC therapeutic applications, where disease or disorder prognosis is related CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell colliferation of stored (e.g. cancer). Another two new methods (M2 and CC M3) are useful for modulating the p53 pathway of a cell, thus restoring CC proliferation or progression through the cell undergoes normal CC also useful for treating defects in the p53 pathway such as angiogenic, CC apoptotic or cell proliferation disorders. (M2) and (M3) are Cell proliferation of special of the cell cycle. (M2) and (M3) are CC apoptotic or cell proliferation disorders. The present sequence CC represents a human p53 pathway modifying present
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CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV
                        CHVP VEKNGGCMIMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV
                                                                        GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
                                                                                               GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
                                                                                                                                                                            LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
                                                                                                                                                 LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
                                                                                                                                                                                                                    CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                                                                                         CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
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nilarity 68.0%;
Conservative
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                                                                                                                                                                                                                                                                                               -----EFFFKCGAHPTSDKETPVALHLIATNSRNITCIT
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Pred. No. 1.8e-140;
0; Mismatches 0;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New
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metabolic irregularity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 40-41; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Luebbert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ew polynucleotides encoding mouse parkin2 protein, useful for producing transgenic non-human animal as an animal model for neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                             GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
                                                                                                                             LHHFRILGEEQYNRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
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GFVFCRDCKEAYHEGDCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPR
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66.0%; Pred. No. 6.3e
tive 14; Mismatches
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.3e-139;
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61 LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLA 120

LEQQSIVHIVQRPRRRSHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLA

MIVFVRENSSHGEPVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD

lqlkevvakrqgvpadqlrvi fagkelpnhltvqncd

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RESULT 13
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Best Local (
Matches 232;
                                                                                                                                                                               6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzhelmer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                           Sequence 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a murine parkin2 polypeptide. The polypucleotide sequence contains a deletion, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 44-45; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding mouse parkin2 a transgenic non-human animal as an animal
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                                                                                                                                                                              Matches
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent: useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIG1676-ABIG1511), expressed DNA sequences (ABIG1675) and the encoded proteins (ABE57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directlem from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 22134; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000; 2000US-00614150
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                                                                     IYVKTNTGKTLTVNLEPQWDİKNVKELVAPQLGLQPDDLKIİFAĞKELSDATTIEQCDLG
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                                      KKTTKPCPRCHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWF
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AAB67519 standard; protein; 250 A

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Amino acid sequence of a murine parkin2 polypeptide

29-MAY-2001

(first

entry)

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XX 10 Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral scle Multi-system atrophy; Wilson's disease; Pick's disease; Prion disea brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity. disease; sclerosis;

EP1081225-A1

07-MAR-2001.

30-AUG-1999; 30-AUG-1999; 99EP-00116766. 99EP-00116766

(BIOF-) BIOFRONTERA PHARM GMBH

Luebbert

N-PSDB; 2001-212797/22. AAF55246

New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative

Claim 7; Page 21-22; 62pp; English.

The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral

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Search completed: February 23, 2005, 13:50:13 Job time: 103.258 secs
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                                                                                                                                                                                                                                                                                                                                                                                                         sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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100.0%; Fred. No. 8.4e-251;
tive 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-844B-4
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APPLICANT: Shimizu, No. 6716621uyoshi

APPLICANT: Shimizu, Yoshikuni

TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease

FILE REFERENCE: 0652.211000

CURRENT APPLICATION NUMBER: US/09/601,844B

CURRENT FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: PCT/JP99/00545

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin version 3.1

LENCTH. 127
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Best Local Similarity 94.0%;
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GENERAL INFORMATION
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                                                                                                      361 GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
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                                             CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV 465

    NÍ VÝVRÉNISSHGÉ PÝVEVDSDTSTĚGÍ KEVVÁKRÓG VÉADÓLKÝ Í FAGKELKNOWTVONCO

                                                                                 ĠPĀPĊĸĖĊĶĒĄŶĤĔĠĖĊŚĄVPĖĄŠĠŦŦŤQĄŶŖVĎĖĸĄĄĔQĄŔŴĔĄĄŚĶĖŦĬĶĶŦŦĶPĊPŖ
                                                                                                                                              LHHFRÍLGÉBÓYNRÝQOYGÁBECVLOMGGVLCÞRÞGCGÁGLLÞBÞDQRKVTCEGGNGLGC
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Pred. No. 9.6e-232;
O; Mismatches O; Indels 2
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RESULT 3 US-09-601-844B-4 Sequence Application US/09601844B

Sequence 683, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CLOCA107

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SES

THEREOF

US-09-949-016-6853

us-10-622-817-9.rai

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 437
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6853
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US-09-949-016-6854
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      Query Match
Best Local Similarity
Matches 316; Conserv
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Crai
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SEQ ID NO 6853
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                                                                     ORGANISM: Human
-09-949-016-6854
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERNCE: CLOO1307
                                                                                                    LENGTH: 316
TYPE: PRT
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94.0%;
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                            68.0%;
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Pred. No. 9.6e-232;
0; Mismatches 0;
                            Score 1696.5;
Pred. No. 4.26
                Mismatches
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                            .2e-161;
                                          DB 4;
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OF DETECTION AND
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                                          Length 316;
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Sequence 13, Application US/09914259
Patent No. 6495336
GRMERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 32183

LENGTH: 117

TYPE: PAT

ORGANISM: Drosophila melanogaster
US-09-270-767-32183
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US-09-270-767-32183
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                                                                                                                                                Matches
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                   404 EAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWF
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                                                                                                                                                                 Similarity
DEASNVTIKVSTKPCPKCRTPTERDGGCMHMVCTRAGCGFEWCWVCQTEWTRDCMGAHWF
                                                                     PDCRKVTCKN----GCGYVFCKNCLQGYHIGECLPEGTGASATNSCEYTVDPNRAAEARW
                                                                                            PDQRKVTCEGGNGLGCGFAFCRECKEAYHEGEC-SAVFEASGTTTQAYRVDERAAEQARW
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                                                                                                                                                Conservative
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                                                                                                                                            14.3%; Score 370.5; DB 4
53.3%; Pred. No. 3.8e-29;
tive 11; Mismatches 40
                                                                                                                                                                                  DB 4;
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                                    463
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 116
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Sequence 2, Application US/09354221
Fatent No. 6699714
GENERAL INFORMATION:
APPLICANT: Chang, Chawnshang
ITITLE OF INVENTION: Androgen Receptor Coactivators
FILE REFERRICE: 920920, 90011
CURRENT APPLICATION NUMBER: US/09/354,221
CURRENT FILING DATE: 1999-07-15
EARLIER APPLICATION WUMBER: US 60/100,243
NUMBER OF SEQ ID DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 12
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; ORGANISM: Homo sapien
US-09-354-221-2
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US-09-354-221-2
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CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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ORGANISM: Drosophila
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                                                                                                                                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  443 LEWCWNCGCEWNRVCMGDHWFD 464
                                                                                                                                                                                                                                                                                                                                       474
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                             LPVMQEPG-----CTMGICSSCNFAFCTLCRLTYHGVSPCKVTAEKLMDLRNEYLQADEA 370
                                                                                                                                                                                                                                            Similarity
-----RVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQPQCRLE 444
                                                         AGLLPEPDQRKVTCEGGNGLGCGFAFCRECKEAYH-EGECSAVFEASGTTTQAY-----
                                                                                      ĆĿ-NĊPBPKCPSVATPGQVKĖĖ----VEABLFARYDRLLLQSSLDLMADVVYĊPKPCCQ 315
                                                                                                                   CVAGCPN-----SLIKELHHFRILGEEQYNRYQQYGAEECVLQMGGVL-CPRPGCG 338
                                                                                                                                                  NSKLFLCSICFCEKLGSECMYFLEC--RHVYCKACLKDYFEIQIRDGQ------VQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNQLĹRWCÞSVDCTYÁVKVÞYAEÞRRVHCK-----CGHVÞCFACGENWHDÞVKCRWL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KKWIKKCDDDSETSNWIAAN-----TKECPRCSVTIEKDGGCNHMVCKNQNCK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STK-----IVAEGLÓQTISCAAHĠC-DILVDDVTVANLVTDARVRVKYQQLITNSFV-E 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VȚRLNDROFVHDPQLGYSLPCVA-GCENSLIKELHHFRILGEEQYN-RYQQYGAEECVLQ 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFKCGAHPTSDKETFVALHLIATNSRNITCITCTDVRSPVLVFQCNSRHVICLDCFHLYC
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27.8%; Pred. No. 2e-13;
ative 27; Mismatches
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-248-796A-15410
GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING '

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1990-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13
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Patent No. 6747137
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US-09-949-016-10111
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US-09-949-016-10111
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 NSRNITC--ITCTDVRSPVLVF-QCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGLLPEPDORKVTCEGGNGLGCGFAFCRECKEAYH-EGECSAVFEASGTTTQAY----- 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARCCHI-----CTIKETHHEKITGEEGANKAGOAGABECATOWGGAT-CEKEGCG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RVDERAAEQARWEAASKETIKKTIKPCPRCHVPVEKNGGCMHMKCPQPQCRLE 444
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27.8%; Pred. No. 2e-13;
Conservative 27; Mismatches
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Maximum Match 100%
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Maximum DB
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    870
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seq length: 2000000000
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2: /cgn2-6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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Match Length
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114.4
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9.5
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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16 US-10-473-226-2
16 US-10-776-604-2
17 US-10-839-689-9
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12 US-10-437-963-139787
13 US-10-080-608A-13
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Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
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Sequence 2, Appli
Sequence 10, Appli
Sequence 17, Appli
Sequence 199787,
Sequence 55407, A
Sequence 55407, A
Sequence 13, Appl
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Sequence 40231, A	0	e 54725	Sequence 152161,	e 18465	e 1245	e 56467	æ	e 5624	e 11137	e 2652	e 330,	e 56,	Ф	e 217	æ	e 140793	æ	e 39657,	æ	æ	æ	æ	e 1824, A	O	3019, A	e 572, Ap	2	42,	e 633	e 14767	Sequence 102, App

ALIGNMENTS

Sequence 2, Application US/10473226 Publication No. US20040198650A1 GENERAL INFORMATION:

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APPLICANT: NaGene A/S
TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin
TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin
FILE REFERENCE: 506-204-WO
CURRENT APPLICATION NUMBER: US/10/473,226
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US 60/281,286
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO
SEQ ID NO
SEQ ID NO
LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (1)...()
OTHER INFORMATION: Native Parkin

OPPER INFORMATION: Native Parkin

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Sequence 2, Application US/10776604
Publication No. US20050003385A1
GENERAL INFORMATION:
APPLICANT: Shimizu, Nobuyoshi
APPLICANT: Mizuno, Yoshikuni
ITILE OF INVENTION: DMAs or Genes Participating in Parkinson's Disease
CURRENT APPLICATION NUMBER: US/10/776,604
PRIOR APPLICATION NUMBER: 09/601,844
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR FILING DATE: 2000-09
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: DF 10/27531
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
IENGTH. 446
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
US-10-776-604-2
                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 2596; DB 16; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.2e-220;
Matches 465; Conservative 0; Mismatches 0; Indels 0;
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US-10-776-604-2
241 CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE 300
                                                                                                                   121 VILHTDSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP 180
                                                                                                                                                            1 MIVFVRFNSSHGFFVEVDSDTSIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCD
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                                                    SCWDDVLIPNRWSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCIT 240
                                                                                              vilhtbskkbspbadspadksivnspyvyckdpcdkvópdklhvócstckdatltiltogp 180
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                                 ŚĆWDĎVĹÍ PŇŔŃŚĠĠĊĢŚPĤĊPĠŤŚAĔŖŖŖĸĊĠĂĤŔŤŚĎĶĔŤŖVAĽĤĹĬAŤŇŚŖNÍŤĊĬŤ
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Publication No. US20050014173A1

GENERAL INFORMATION:

APPLICANT: FATE'EY, Matthew J.

TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS
FILE REFERENCE: 07039-448001

CURRENT APPLICATION NUMBER: US/10/839,688

CURRENT FILING DATE: 2004-05-05

PRIOR APPLICATION NUMBER: US 60/468,832

PRIOR TILING DATE: 2003-05-08

PRIOR PILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PASTSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Homo sapiens
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                        421 CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWPDV 465
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       CHVPVEKNOGCMIMKCPOPOCRLEWCWNOGCEWNRVCMGDIWFDV 465
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                                                                GPÁPČKEČKEÁYHEGEĆSÁVPEÁŚGTTTQÁYRVDERÁÁEQÁRWEÁÁSKETIKKTTKPČPR
                                                                                    GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR 420
                                                                                                                                LHHFRÍLGÉBÓYNRÝOOYGAEBCVLOMGGVLĆFRÞGCGAGLLFBFDORKVTCEGGNGLGC
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                                                                                                                                                                                                                                                                SCWDDVLÍPNRMSGÉCOSPHCPGTSAEFFFRCGAHPTSDKETPVALHLÍATNSRNÍTCÍT
                                                                                                                                                                                                                                                                                   SCWDDVLIPNRMSGECOSPHCPGTSAEFFFKCGAHPTSDKETFVALHLIATNSRNITCIT
                                                                                                                                                                                                                                                                                                                            VILHTDŚRKDŚPPAGŚPAGKŚIYNSPYVYCKĠPĆÓRVĄPGKLKVĄĆSTĆRQATLTLTĄGP
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Indels Length 465;

0;

Gaps

0

120

60 60 문 Ś 뭐 Ś 밁 Ś 문 Ś B Ś 밁 Ş 밁

Ś В Ş 밁 Ş 밁 Ś

181 181

420

360 360 300

240 240 180 180

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RESULT 5
US-10-776-604-4
; Bequence 4, Application US/10776604
; Publication No. US20050003385A1
; GENERAL INFORMATION:
; APPLICANT: Shimizu, Nobuyoshi
; APPLICANT: Mizuno, Yoshikuni
; TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease
; FILE REFERENCE: 0652.2110001
; CURRENT APPLICATION NUMBER: US/10/776,604
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APPLICANT: NBGene A/S
TITLE OF INVENTION: Means for inhibiting proteolytical processing of
FILE REFERENCE: 506-204-WO
CURRENT APPLICATION NUMBER: US/10/473,226
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: DK PA 2001 00525
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 7
ROPERATOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.5%;
Best Local Similarity 99.6%;
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LOCATION: (1)..()
OTHER INFORMATION: Parkin with a D126E mutation
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TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
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Pred. No. 2.5e-219;
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Sequence 4. Application US/0978548

Patent No. US20020155577A1

GENERAL INFORMATION: PHARMACEUTICALS, INC.

PILL REPERENCE: STOODOS

CURRENT APPLICATION UNMBER: US/09/785,548

CURRENT FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 46

SOFTMARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 156

TYPE: PRT

ORGANISM: Homo sapiens

US-09-785-548-4
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 437
TYPE: PRT
ORGANISM: Homo sapiens
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Query Match
Best Local Similarity
Matches 155; Conserv
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Best Local
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PRIOR APPLICATION NUMBER: 09/601,844
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR TILING DATE: 1999-02-09
PRIOR PILING DATE: 1998-02-09
PRIOR RELIGION NUMBER: JP 10/27531
PRIOR FILING DATE: 1998-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKB
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 33.5%;
ilarity 99.4%;
Conservative
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Score 870; DB 9;
Pred. No. 1.3e-68;
0; Mismatches 1
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Pred. No. 1.5e-203;
0; Mismatches 0;
                                                                                                                                                                                                                                          USED FOR REGULATING THE ACTIVITY OF PARKS
                                 Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 437;
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GENERAL INFORMATION:

APPLICANT: HONER, MARIUS

APPLICANT: HONER, MARIUS

APPLICANT: HONER, MARIUS

APPLICANT: HONER, MARIUS

APPLICANT: HONER, MARIUS

APPLICANT: HONER, MARIUS

APPLICANT: HONER, MARIUS

APPLICANT: BAUMEISTER, RALF

ITITLE OF INVENTION: NEWATODES AS MODEL ORGANISMS FOR INVESTIGATING

ITITLE OF INVENTION: DISEASE, USES AND METHODS FOR FINDING SUBSTANCES AND

ITITLE OF INVENTION: DISEASE, USES AND METHODS FOR FINDING SUBSTANCES AND

ITITLE OF INVENTION: DISEASE, USES AND METHODS FOR FINDING SUBSTANCES AND

ITITLE OF INVENTION: DISEASE, USES AND METHODS FOR FINDING SUBSTANCES AND

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US-10-239-249-2
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Publication No. US20030177507A1
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                                                    SAVFEASGTTTOAYRVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHNKCP 437
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                                                                                                                                                                  EECV-LOMGGVLCPRPGCGAGLLPEP--DORKVTCEGGNGLGCGFAFCRECKEAYHEGEC 377
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-TIDATTRRCPKCHVATERNGGCAHIHC- 360
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RESULT 10
US-09-864-761-36750
; Sequence 36750, Application US/09864761
; Patent No. US20020048763A1
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US-10-313-203-17
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APPLICANT: GI, Wei
APPLICANT: Nikolaev, Anatoly
ITILE OF INVENTION: P53-ASSOCIATED PARKIN-LIKE CYTOPLASMIC PROTEIN, AND RELATED COMPO
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ITILE OF INVENTION: MUMBER: US/10/313,203
ICURRENT APPLICATION NUMBER: US/10/313,203
ICURRENT FILING DATE: 2002-12-06
INUMBER OF SEQ ID NOS: 30
ISOFTWARE: Patentin version 3.1
ISEQ ID NO 10
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Publication No. US20040029134A1
GENERAL INFORMATION:
APPLICANT: GL, Wei
APPLICANT: Nikolaev, Anatoly
TITLE OF INVENTION: P53-ASSOCIATED PARKIN-LIKE CYTOPLASMIC PROTEIN, AND RELATED COMPOSE FILE REFERENCE: 68106
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 302-12-06
NUMBER OF SEQ ID NOS: 302-12-06
SCOPTWARE: Datentin varion 1
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US-10-313-203-10
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Publication No. US20040029134A1
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100.0%; Pred. No. 3e-25;
tive 0; Mismatches 0;
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Maximum Match 100%
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Copyright (c) 1993 - 2005 Compugen Ltd.
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QY 379 AVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPRCHVPVEKNGGCMHMKCPQ	Qy 322 ECV-LQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGCGFAFCRECKEAYHEGECS -:	OY 262 DCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKELHHFRILGEEQYNRYQQYGAE	Qy 202 PGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCITCTDVRSPVLVFQCNSRHVICL	OY 142 IYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGPSCWDDVLIPNRMSGECQSPHC	Oy 82 ATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLAVILHTDSRKDSPPAGSPAGRS	Qy 22 SIFQLKEVVAKRQGVPADQLRVIFAGKELRNDWTVQNCDLDQQSIVHIVQRPWRKGQEMN	Query Match 18.9%; Score 490; DB 2; Lenger Best Local Similarity 26.7%; Pred. No. 1.8e-29; Matches 119; Conservative 53; Mismatches 154; I.	GNMENTS bditis ele 15-Oct-199 ember 1996 GB/EMBL/DI GB/EMBL/DI	133 5.1 397
TIKKTTKPCPRCHVEVEKNGGCMHMKCPQ 438 : : : : TIDATTRRCPKCHVATERNGGCAHIHC 331	GFAFCRECKEAYHEGECS 378 : : sFSFCRKCFERNCV 294	NSLIKELHHFRILGEEQYNRYQQYGAE 321 	VRSPYLVFQCNSRHVICL 261	DDVLIPNRMSGECQSPHC 201	HTDSRKDSPPAGSPAGRS 141	OSIVHIVQRPWRKGQEMN 81	Length 357; Indels 120; Gaps 12;	VIDI receptor VIDI receptor ORP MSY144 pro probable ubiqu polyubiquitin protein T19E2: polyubiquitin polyubiquitin polyubiquitin polyubiquitin polyubiquitin exte ubiquitin exte ubiquitin exte polyubiquitin exte ubiquitin exte	probable RING zinc

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R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. DNA Res. 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete A;Reference number: Z14142; MUID:98403880; PMID:9734611
A;Accession: T00350
                                                                                                                                                                                                                        A;Status: preliminary; translated fr
A;Molecule type: mRNA
A;Residues: 1-1753 <1SH
A;Cross-references: UNIPROT: Q8IWT3;
                                                                                                                                                                                                    A; Experimental source: brain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein KIAA0708 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                 A;Note: KIAA0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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A;MOlecule type: DNA
A;Molecule type: DNA
A;Residues: 1-543 <STO>
A.Cross-references: UNIPROT:Q9SKC3; GB:AE002093; NID:g4887759; PIDN:AAD32295.1; GSPDB:GN
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                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: H84724
R; Lin, X.; Kaul, S.;
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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                  MWLLLKFNOTBEVSVETLLKDSDLSPELLLQALVPLTSGNGPLTLHEGQDFPHGGVLRLH 1071
                                                              MIVFVRFNSSHGFPVEV---DSDTS-----
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25.9%; Pred. No. 5.9e-09;
ative 33; Mismatches 83
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Pred. No. 2.2e-
57; Mismatches
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A;Introns: 41/3; 134/3; 185/3; 223/3; 254/2; 287/2; 414/3
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q20871; ENA;Experimental source: strain Bristol C;Genetics:
                                                                                                                                                                                                                                                                                                               A; Gene: CESP: F56D2.5
                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-437 < DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: The sequence A;Reference number: Z18519 A;Accession: T16477
                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, August 1994 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F56D2.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T16477
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136 SPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGPSCWDDVLIPNRMSGE
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                                                                                                                                         DSDTSIFQLKEVVAKRQGVPADQLRVIFAGKEL--RNDWTVQNCDLDQQSIVHIVQRPWR 75
                                                 ------GPDNLYDPTVTIEGTSDSGDQFHLPLDILP-----PIRLKFHLPNDYPTVS
                                                                                 KGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGLAVILHTDSRKDSPPAG
                                                                                                                                    DRDLQIYEL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEKALLRGY-VESC---SNLTWCTNPQGCD-----RILCRQGLGCGTTCSKCGWA 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQQ-----YGAEECVLQMGGVLCPRP-GCGAGLLPEPDQRKVTCEGGNGLG-----CGFA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKSCWNEYLTTRI-----EQNLVLNCTCPIADCPAQPTGAFIRAI----VSSPEVISK 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLDCFHLYCVTRLNDRQFVHDPQLGYSLPC-VAGCP----NSLIKELHHFRILGEEQYNR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCWDDVLIPNRMSGECQSpHCPGTSAEFFFK---CGAHPTSDKETPVALHLIATNS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRKDSPP-----AGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP 180
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                 7.9%;
20.2%;
                                                                                                                                                                                            66; Mismatches 169; Indels
                                                                                                                                                                                                               Score 205; DB 2;
Pred. No. 6.3e-08;
                                                                                                                    -EALESVLREKKLAKSSDWSDKNAEI--QGIIEV-----
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ol N2; clone F56D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RNITCITCTDVRSPV----LVFQCNSRHVI 259
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                                                                                                                                                                                                                                Length 437;
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Result
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: uniprot_trembl:*
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  GenCore version 5.1.6 (c) 1993 - 2005 Compus
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Q8CGU7
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ARI1 MOUSE
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ARI2 MOUSE
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PRKN_RAT
PRKN_MOUSE
                                                                                                                                                                                                                           Q68F65
Q653S8
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Q95MI4
Q95MI4
Q7KTX7
Q7Q591
Q7Q591
Q8NI41
Q8K5C2
Q9XUS3
Q86LE7
Q8VHY5
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             Hattori N.,
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PubMed=12925569; DOI=10.1093/hmg/ddg269; Huynh D.P., Scoles D.R., Nguyen D., Pulst S. "The autosomal recessive juvenile Parkinson parkin, interacts with and ubiquitinates synthm. Mol. Genet. 12:2587-2597(2003).
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NOOKes A.J., Yamamura Y., Kobayashi T.,
Minoshima S., Shimizu N., Mizuno Y.;
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ng F., Becker N.A., (
lein C., Smith D.I.;
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Schneider R., Mizuno Y., Kosik
E a new form of alpha-symuclein
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, Mizuno Y.;
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Q93K56; Q8K5C3; Q8K5C4; Q8K5C5; Q8K5C6; Q8VHY6;
25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Parkin (EC 6.3.2.-) (Ubiquitin E3 ligase PRKN)
Name=Park2; Synonyms=Prkn;
                                                                          MEDLINE 20199898; PubMed-10737637;
GU W.-J., Abbas N., Lagunes M.Z., Parent A., Pradier L., E
Agid Y., Hirsch E.C., Raisman-Vozari R., Brice A.;
"Cloning of rat parkin cDNA and distribution of parkin in
J. Neurochem. 74:1773-1776(2000).
                                                                                                                                                                                                STRAIN-Sprague-Dawley;

MEDLINE-20153712; PubMed=10686358; DOI=10.1016/S0169-328X(99)00286-7;

D'Agète V. Zhao W. Cavallaro S.;

"Cloning and distribution of the rat parkin mRNA.";

Brain Res. Mol. Brain Res. 75:345-349(2000).
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                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                               STRAIN-Sprague-Dawley;
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                                                 SEQUENCE FROM N.A.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Functions within a multiprotein E3 ubiquitin ligase
                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
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                                                                                                                                   Event=Alternative splicing; Named isoforms=6;
                                                                                           IsoId=Q9JK66-5;
                                                                                                   IsoId=Q9JK66-4;
                                                                                                           IsoId=Q9JK66-3;
                                                                                                                   IsoId=Q9JK66-2;
                                                                                                                           IsoId=Q9JK66-1; Sequence=Displayed;
           found by any domain detection methods.
                                                                                                                                                                                                                                                                             Imai Y., Takahashi R.
                                                                                                                                                                                                                                                                                     FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                            (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                           Sequence=VSP_011719;
                                                                                                           Sequence=VSP_011717;
                                                                                                  Sequence=VSP_011718;
                                                                                                                   Sequence=VSP_011722,
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InterPro; IPR000626; Ubiquitin.

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InterPro; IPR002667; Znf C6HC.

Pfam; PF01485; IBR; 1.

PFANYIS; PR01475; PARKIN.

PRINTS; PR01475; PARKIN.

PRINTS; PR00340; UBIQUITIN.

SMART; SM00647; IBR; 2.

SMART; SM00647; IBR; 2.

SMART; SM00213; UBQ; 1.

PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.

PROSITE; PS0053; UBIQUITIN_2; 1.

Alternative splicing; Ligase; Metal-binding; Repearation onjugation; Dathway; Zinc; Zinchart
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PubMed=12652124;
PubMed=12652124;
Tashiro M., Okubo S., Shimotakahara S.,
Kainosho M., Yokoyama S., Shindo H.;
"NMR structure of ubiquitin-like domain
                                                                                                                           Dawson V.L., Dawson T.M.,
"S-nitrosylation of parkin reparkin's protective function.
Science 304:1328-1331(2004).
                                                                                                                                                                                      FUNCTION IN UBIQUITINATION, AND S-NITROSYLATION.
PubMed=15105460; DOI=10.1126/Science.1093891;
Chung K.K., Thomas B., Li X., Pletnikova O., Tro
Dawson V.L., Dawson T.M.;
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MEDLINE-20571394; PubMed-11122330;
Stichel C.C., Augustin M., Kuehn K
                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY PubMed=11675120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitada T., Asakawa S., Minoshima S., "Molecular cloning, gene expression, variant of the mouse parkin gene."; Mamm. Genome 11:417-421(2000).
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25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Parkin (EC 6.3.2.-) (Ubiquitin E3 ligase PRKN)
Name=Park2; Synonyms=Prkn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
LOCATION.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PubMed=10818204;
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MOD

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IsoId=Q9NVS6-3; Sequence=VSP 011716;
-ITISQUE SPECIFICITY: Expressed In all subdivisions of the brain.
Highly expressed in brainstem, cranial nerve, pontine, cerebellar nuclei, indusium grieeum, nuclei reticularis, strata oriens and laccunosum moleculare of the hippocampal CA2 region. Low levels were found in the telencephalon and diencephalon. Expressed in heart, liver, skeletal muscle, kidney and testis.

-IDEVELOPMENTAL STAGE: In late 10 dpc weakly expressed in postmitotic neurons in the mantle layer of the developing nervous system. Expression increased at 11-12 dpc. At 15-16 dpc, as more specific expression was highest in the neurites, moderate levels were observed in the migrating postmitotic neurons in the intermediate and neopallial layers. In the diencephalon and other CNS regions, while the weakest level of expression was observed in the cell bodies. In nonneural tissues, high levels of expression were found in the muscle walls of the intestine, the blood vessels and the dermis.

-IDMAIN: The ubiquitinates in an E2-dependent manner leading to its own degradation (By similarity).

-IPTM: Sunitarity: Contains 2 IBR-type zinc fingers.
-ISMILARITY: Contains 2 IBR-type zinc fingers, but these are not found by any domain detection methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biomol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      familial Parkinson's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Functions within a multiprotein E3 ubiquitin ligase complex, catalyzing the covalent attachment of ubiquitin moieties onto substrate proteins. These substrates include SYT11, CCNE1, oppositions, STUB1, a 22 kDa O-linked glycosylated isoform of SNCAIP and SEPTS. May play a more general role in the ubiquitin proteasomal pathway by participating in the removal and/or detoxification of abnormally folded or damaged protein. Loss of this ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     postsynaptic densities. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event-Alternative splicing; Named isoforms=3;
                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9WVS6-2; Sequence=VSP_011714, VSP_011715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9WVS6-3; Sequence=VSP_011713, VSP_011716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9WVS6-1;
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CHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV

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PRINTS; PRO0346; UBLQUITIN.
SMART; SM00647; IBB; 2.
SMART; SM00213; UBQ; 1.
PROSITE; PS00299; UBLQUITIN
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-structure; Alternative splicing; Ligase; Metal-binding; Repeat; S-nitrosylation; Ubl conjugation; Ubl conjugation pathway; Zinc;
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Pfam; PF00240; ubiquitin; 1.
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PROSITE; PS50053; UBIQUITIN_2; 1.
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MGD; MGI:1355296; Park
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InterPro; IPR000626; Ubiquitin.
InterPro; IPR002867; Znf_C6HC.
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AF250293; AAG13890.1; -.
AF250294; AAG13891.1; -.
AF250295; AAG13892.1; -.
                                                                                                                                                                                                                                                                                                                                        388;
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                GFAFCRECKEAYHEGECSAVFEASGTTTQAYRVDERAAEQARWEAASKETIKKTTKPCPR
                                                                   LHHFRILGEEQYNRYQQYGABECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGC
                                                                                                         CTDVRSPVLVFQCNSRHVICLDCFHLYCVTRLNDRQFVHDPQLGYSLPCVAGCPNSLIKE
                                                                                                                                                                   SCWDDVLIPNRMSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCIT
                                                                                                                                                                                                                 VILHTDSRKDSPPAGSPAGRSIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATLTLTQGP
                                                                                                                                                                                                                                                          LDQQSIVHIVQRPWRKGQEMNATGGDDPRNAAGGCEREPQSLTRVDLSSSVLPGDSVGIA 120
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  GFVFCRDCKEAYHEGDCDSLLEPSGATSQAYRVDKRAAEQARWEEASKETIKKTTKPCPR
                                                LHHFRILGEEQYTRYQQYGAEECVLQMGGVLCPRPGCGAGLLPEQGQRKVTCEGGNGLGC
                                                                                              CTDVRSPVLVFQCNHRHVICLDCFHLYCVTRLNDRQFVHDAQLGYSLPCVAGCPNSLIKE
                                                                                                                                              SCWDDVLIPNRMSGECOSPDCPGTRAEFFFKCGAHPTSDKDTSVALNLITSNRRSIPCIA
                                                                                                                                                                                             VILDTDSKRDSEAARGPV-KPTYNSFFIYCKGPCHKVQPGKLRVQCGTCKQATLTLAQGP
                                                                                                                                                                                                                                           LEQQSIVHIVQRPRRRSHETNASGGDEPQSTSEGSIWESRSLTRVDLSSHTLPVDSVGLA
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STY11 binding 1.
STY11 binding 2.
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9; Mismatches 47;
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/FTId=\Sp 011716.

P -> PA (In Ref. 1 and 2; AAG13890)

5574A285A9A1B080 CRC64;
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Missing (In isofo
/FTId=VSP_011715.
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SPVLVFQCNH -> FM
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Best Local Sim
Matches 198;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, AF3981284; AAM21459.1; --
R GO; GO:0004842; F:ubiquitin.protein ligase activity; IEA.
R GO; GO:0006512; P:ubiquitin cycle; IEA.
R GO:0006512; P:ubiquitin cycle; IEA.
R InterPro; IPR003977; parkin.
R InterPro; IPR002867; Znf_C6HC.
R InterPro; IPR002867; Znf_C6HC.
R PFAMT; PR01485; IER; 1.
R PFAMT; SM00647; IBR; 1.
R SMART; SM00647; IBR; 1.
R SMART; SM00647; IBR; 1.
                                                                                                                                                                                                                                                                                                                                                             Q95M07 PRELIMINARY;
Q95M07;
01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-JUN-2003 (TrEMBLrel. 24, L
Parkin (Fragment).
                                                                                                                                                                                                                                                                 Name=parkin gene;
Bos taurus (Bovine).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
                    MEDLINE=98219084; PubMed=9560156; DOI=10.1038/33416; Kitada T., Asakawa S., Hattori N., Matsumine H., Yamamura Minoshima S., Yokochi M., Mizuno Y., Shimizu N.; "Mutations in the parkin gene cause autosomal recessive juparkinsonism.";
                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                 Bovinae; Bos.
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Q8NI42,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Parkin isoform.
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                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Last sequence up
Last annotation
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; Pred. No. 1.2e-79; Pred. No. 1.2e-79; O;
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A Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

A Stapleton M., Chavez C., Dorsett V., Farfan D., Frise E., George R

A Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R

A Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.

A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan

A Yu C., Lewis S.E., Rubin G.M., Celniker S.;

L Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AY058754, AAL13983.1; -.

R HMBL, AY058754, AAL13983.1; -.

R HMBL, BYDG874; TAAR.

R FlyBase; FBgn0041100; park.

R GO; GO:0007005; P:mitochondrion organization and biogenesis; IM

THTATPTO. TPRO20252; N6 Mtase.
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Matches 193
Pfam; PF01485; IBR; 1. — Pfam; PF00240; ubiquitin; 1. PRINTS; PR01475; PARKIN. PRINTS; PR00348; UBIQUITIN. SMART; SM00647; IBR; 2. SMART; SM00213; UBQ; 1.
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01-DEC-2001
01-MAR-2004
SD01679p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=park; Synonyms=CG10523;
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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EMBL; AB660701; BAB70670.1; -.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IER003977; parkin.
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                                                                                                                                           IPR003977; parkin.
IPR000626; Ubiquitin.
IPR002867; Znf_C6HC.
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21225 MW;
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Pred. No. 2.4e-75;
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2. gb_tr

3. gb_in

4. gb_or

5. gb_or

6. gb_r

7. gb
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AR492172 Sequence
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AX584226 Sequence
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AB009973 Homo sapi
BC022014 Homo sapi
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1 GGAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCTGTTGT	ફ ફ
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/ Match 100.0%; Score 471; DB 6; Length 471; Local Similarity 100.0%; Pred. No. 2.3e-143; nes 471; Conservative 0; Mismatches 0; Indels 0; Gaps	Query Match Best Local : Matches 47:
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	source
Location/Qualifiers	FEATURES
RECHERCHE MEDICALE (INSERM) (FR)	
	JOURNAL
Arnould-Reguigne, I., Rosier-Montus, M.F. and Corti, O.	4.141.E
Koutnikova, H., Brice	AUTHORS
1	REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Homo sapiens	ORGANISM
Homo sapiens (human)	SOURCE
WY524452:1 G1:12234002	VERSTON
AX224425	ACCESSION
N Sequence 3 from Patent WO0160857.	DEFINITION
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2960)
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tions of the parkin gene, compositions, methods and uses F
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source 1. .2960
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C12N15/09, A01K67/027, C07K14/47, C07K16/18, C12N1/15, C12N1/19,
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JP 2002536961-A/1
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19-NOV-1998 FR 98/14524,12-MAR-1999 US
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                                                                                                                                /organism='Homo
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2 (bases 1 to 904)
D'Agata,V., Scapagnini,G. and Cavallaro,S.
Direct Submission
Submitted (01-MAY-2001) Institute of Bioimaging of the Central Nervous System, Italian National (CNR), Piazza Roma, 2, Catania 95123, Italy
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1 (Dases 1 to 904)

D'Agata,V., Scapagnini,G. and Cavallaro,S.
Functional and molecular diversity of parkin
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                  /product="parkin isoform"
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CWDDVLJPNRMSGECQSPHCPGTSAEFFFKCGAHPTSDKETPVALHLIATNSRNITCI
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74...730
                                                                                                                          /note="alternatively spliced; transcript variant
/codon_start=1
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and Pathophysiology Research Council

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                                                                                                                                                            Unclassified.

1 (bases 1 to 2960)
1 (bases 1 to 2960)
Shimizu, N. and Mizuno, Y.
Isolated DNA or gene responsible for Parkinson's disease
Patent: US 6716631-A 1 06-APR-2004;
Location/Qualifiers
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Sequence 1 f
AR492172
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         ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
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                                                                                                                                               /organism="unknown"
/mol_type="genomic"
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patent US 6716621.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 1 from Patent P
AX584224
AX584224.1 GI:27655742
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AACATCACTTGCATTACGTGCACAGACGTCAGAGGCCCCGTCCTGGTTTTCCAGTGCAAC
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                                                                               GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTTCTTTAAATGTGGAGCA
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ilarity 99.8%;
Conservative
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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Patent WO02079459.
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Pred. No. 9.6e-142;
0; Mismatches 1;
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AX584226
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                                                               GGCAGTTTGTTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGTG
                                                                             CGGCAGTTTGTTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGTG 468
                                                                                                              TCCCGCCACGTGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGAT
                                                                                                                              aacarcacrigearracerecacaeacercaeeaecececerecreerriceaeinecaae
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Mammalia; Eutheria; Primates;
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3 from Patent WO02079459.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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2 (bases 1 to 2960)
3 (bases 1 to 2960)
Shimizu,N., Kitada,T. and Asakawa,S.
Shimizu,N., Kitada,T. and Asakawa,S.
Direct Submission
Direct Submission
Submitted (22-DEC-1997) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuki-ku, Tokyo 160-8582, Uspan
Shinjuki-ku, Tokyo 160-8582, Uspan
Shinjuki-ku, Tokyo 160-8582, Uspan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitada, T., Asakawa, S., Hattori, N., Matsumine, H., Y Minoshima, S., Yokochi, M., Mizuno, Y. and Shimizu, N. Mutations in the parkin gene cause autosomal reces parkinsonism Mature 392 (6676), 605-608 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (E-mail:shimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370(ex.2720)
Fax:81-3-3351-2370)
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/db_xref="taxon:9606"
/chromosome="6"
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mol_type="mRNA"
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Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1575)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Parmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyai,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
Abramson,R.D., Malek,J.A., Gunaratne,P.H., Richards,S.,
                                                                                                                                                                                                                                                                        1575 bp mRNA linear i
Homo sapiens Parkinson disease (autosomal recessive,
parkin, mRNA (cDNA clone MGC:26491 IMAGE:4824892), cc
BC022214
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
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/gene="parkin"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4758883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced
Contact: MGC help desk
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Na
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Institute for Systems http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Madan, Stephanie Rodrigues, Amy Sanchez a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Direct Submission
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SHETTEN ATTORNAM TOTTOTTURASPVLVPQCNSHLIKELHHFRILGEEQYNRY
QYGABECVLQMGGVLCPRPGCGAGLLPEPDQRKVTCEGGNGLGCGYGQRRTK"

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proteins: SUMO (smt3

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DEFINITION
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D'Ageta,V., Scapagnini,G. and Cavallaro,S.
Direct Submission
Submitted (01-MAY-2001) Institute of Bioimaging
of the Central Nervous System, Italian National
(CNR), Piazza Roma, 2, Catania 95123, Italy
Location/Qualifiers
                                                                                                                                                                                           D'Agata, V., Scapagnini, G. Functional and molecular compublished
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Pred. No. 3e-141;
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diversity of parkin
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mRNA,
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  Hase,
                                                                                                                                                Kitada, T., Asakawa, S., Hattori, N., Matsumine, H., Minoshima, S., Yokochi, M., Mizuno, Y. and Shimizu, P. Mutations in the parkin gene cause autosomal rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
462; Conserv
                                                  Characterization of Brain Res. 930 (1-2)
                                                                             Hase, A.,
                                                                                                                 Nature 392
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Bos taurus
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Bos taurus mRNA for parkin,
AB060701 GI:16444927
                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                         Bovinae; Bos.
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TIKKTTKPCPRCHVPVEKNGGCMHMKCPQPQCRLEWCWNCGCEWNRVCMGDHWFDV"
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583)
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/protein_id="BAB70670.1"
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/db_xref="01:16444928"
/translation="AGGCEREPOSLIRVDLSSSVLPGDSVGLAVILHTDSRKDSPPAG
/translation="AGGCEREPOSLIRVDLSSSVLPGDSVGLAVILHTDSRKDSPPAG
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GECQSPHCPGTSAEFFEKCGAHPTSDKETSVALHLIATNSRNITCITCTDVRSEVLVF
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2 (bases 1 to 1564)

Hattori,N., Wang,M. and Mizuno,Y.
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                                                                                 ACCCAACCTCAGACAAGGACACATCAGTAGCTTTGAACCTGATCACCAACAACAGCCGCA
                                                                                                             ACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGA
                                                                                                                                                                               AGTGCCAATCTCCAGACTGCCCTGGGACAAGAGCTGAATTTTTCTTTAAATGTGGAGCAC
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VDQRAAEQARWEEASKETIKKTTKPCPRCNVFIEKNGGCMHMKCPQPQCKLEWCWNCG
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/mol_type="mRNA"
/strain="Srague-Dawley"
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Pred. No. 1.4e-104;
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Rattus norv
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AF343575.1
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Submitted (29-JAN-2001) Institute of Bioimaging Submitted (29-JAN-2001) System, Italian National
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1 (bases 1 to 904)
D'Agata, V.M., Scapagnini, G. and Cavallaro, S.
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                               Similarity
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                                    ACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGA
                                                                                     CCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTG
                                                                                                                                                                   ACAAGGTCCAGCCTGGGAAACTCCGAGTTCAGTGCGGCACCTGCAGACAAGCAACCCTCA
ACATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAACT
                                                                                                                      CCTTGGCCCAGGGCCCATCTTGCTGGGATGATGTCTTAATTCCAAACCGGATGAGTGGAG
                                                                                                                                                                                                                     GAGGTCCAGCAACCTAACCACACACACTTTTTTGTCTACTGCAAAGGCCCCTGCC
                                                                       AGTGCCAATCTCCAGACTGCCCTGGGACAAGAGCTGAATTTTTCTTTAAATGTGGAGCAC
                                                                                                                                                                                 ACCCAACCTCAGACAAGGACACATCAGTAGCTTTGAACCTGATCACCAACAACAGCCGCA
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Piazza Roma, 2, Catania 95123, Italy
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="parkin transcript variant
/protein_id="AAL/73349.1"
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PCIACTDVRNPVLVFQCNHRHVICLDCFHLYCVTRLNDRQFVHDAQLGYSLPCVVRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway
Rattus norvegicus
Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Rodent
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D'Agata, V. and Cavallaro, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1466)
D'Agata,V., Zhao,W. and Cavallaro,S.
Cloning and distribution of the rat parkin
Brain Res. Mol. Brain Res. 75 (2), 345-349
                            CCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTG
                                                                                                                             GAGGTCCAGAAGCTAAACCCACCTACCACACACTTTTTTGTCTACTGCAAAGGCCCCTGCC
                                                                                                                                                                                                                         GAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCTGTC
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  CCTTGGCCCAGGGCCCATCTTGCTGGGATGATGTCTTAATTCCAAACCGGATGAGTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MIVFVRFNSSYGFPVEVDSDTSICQLKEVVAKRQGVPADQLRVI FRAKKELQNHLTVQNCDLEQQSIVHIVQRQKKSHETNASGGKPCQSTPRGSIWEPRSL TRVDLSSHLIFADSVGLAVILDTDSKSDSEARAGPBAKPTYHSFFVYCKGFCHKVPGKFCKGAHPTS KLRVQCGTCRQATLTLAQGPSCWDDVLIFNRMSGECQSFDCFGTRAEFFFKCGAHPTS DKDTSVALMLTINNSRSIFCIACTDVRNPVLVFQCNHRHVICLDCFHLYCVTRLNDRQ DKDTSVALMLTNNSRSIFCIACTDVRNPVLVFQCNHRHVICLDCFHLYCVTRLNDRQ
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PGCGAGLLPEQGQKKVTCEGGNGLGCGFVFCRDCKEAYHEGECDSMFEASGATSQAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                             VDQRAAEQARWEEASKETIKKTTKPCPRCNVPIEKNGGCMHMKCPQPQCKLEWCWNCG
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/db_xref="GI;7001384"
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/db_xref="taxon:10116"
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Gu, W.J. and Abbas, N.E.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-DEC-1999) Neurology, INSERM U289, L'Hopital, Paris 75013, France
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Mammalia; Eutheria;
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D'Agata, V.M., Scapag
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CEGGNCLGCGFVFCRDCKEAYHEGECDSMFBASGATSQAYRVDQRAAEGARWEEASKE
TIKKTTKPCPRCNVPIEKNGGCMHMKCPQPQCKLEWCWNCGCEWNRACMGDHWFDV"
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δ	64 AGAGTGCAGCCGGGAAAACTCAGGGTACAGTGCAGCACCTGCAGGCAG	
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Ş	124 TTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTGAA 183	
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δ	184 TGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCACAC 243	
Вb	345 TGCCAATCTCCAGACTGCCCTGGGACAAGAGCTGAATTTTTCTTTAAATGTGGAGCACAC 404	
δ.	244 CCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGAAC 303	
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οy	304 ATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAACTCC 363	
Db	465 ATCCCCTGCATCGCGTGCACGGATGTCAGGAACCCTGTCTTGGTCTTCCAATGTAACCAC 524	
δ	364 CGCCACGTGATTTGCTTAGACTGTTTTCCACTTATACTGTGTGACAAGACTCAATGATCGG 423	
Ф	525 CGCCACGTGATCTGGACTGCCTTCCACTTGTACTGTGTCACAAGGCTCAACGATCGG 584	
89	424 CAGTITGITCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGTG 468	
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Pred. No. 7.8e-153;
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RESULT 3
AXY9923
ID AXY9
XX AXY9
XC AXY9
XC AXY9
XC Huma
XX Huma
XX Park
XX Park
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
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Homo

sapiens

Location/Qualifiers 102. .1499

Parkinson's disease

related

gene; parkin

gene; variant;

gene

therapy;

88

Human 21-OCT-1999 AAX99923;

parkin

gene

variant.

(first

entry)

AAX99923 standard; DNA; 2960

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a cDNA sequence of the human parkin protein gene. The specification describes a parkin gene which has genetic alterations. Cells, or transgenic animals, that express the altered parkin gene are used to screen for compounds that can counter the effects of a genetic alteration in the parkin gene, or more generally for studying the properties of the parkin protein. Detection of the specified alterations is used to diagnose susceptibility to Parkinson's disease. The modified polynucleotide is also used to express the corresponding protein, which is then used to screen for potential anti-Parkinson agents and to raise antibodies (for detecting variants of parkin protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variant forms of the human parkin gene, used as source of primers probes for detecting susceptibility to Parkinson's disease.
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                  CGGCAGTTTGTTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGTG
                                                                                CGGCAGTTTGTTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGTG
                                                                                                                            AACATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAAC
                                                                                                                                                 AACATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTTCCAGTGCAAC
                                                                                                                                                                                                                                                      GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTTCTTTAAATGTGGAGCA
                                                                                                                                                                                                                                                                          GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTTCTTTAAATGTGGAGCA
                                                              TCCCGCCACGTGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGAT
                                                                                                                                                                                          CACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAATAGTCGG
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                                                                                                                                                                                                                                                                                                                    ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                    2960 BP; 815 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.4%; Score 468; DB 3; Lilarity 100.0%; Pred. No. 2.3e-151; Conservative 0; Mismatches 0;
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RESULT 4
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Best Local S
Matches 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a gene of the invention, and is implicated in the pathology of Parkinson's disease. This sequence is a variant of the parkin gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene implicated in the pathology of Parkinson's treatment of the disease.
  AAD47679;
                         AAD47679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2960 BP; 815 A; 727 C; 698 G; 720 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-1998;
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467; Conserv
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                         standard; cDNA; 2960
                                                                                                                                                                                                   AACATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGGTCCTGGTTTTCCAGTGCAAC 360
                                                                                                                                                                                                                                                     CACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGG
                                                                                                                                                                                                                                                                                        GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCA
                                                                                                                                                                                                                                                                                                   GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCA
                                                                                                                                                                                                                                                                                                                                                      ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                          CANAGAGTGCAGCCGGGANAACTCAGGGTACAGTGCAGCACCTGCAGGCAGGCAACGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCCTGT 60
                                                                                                           CGGCAGTTTGTTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGTG 468
                                                                                                                                                              TCCCGCCACGTGATTTGCTTAGACTGTTTTCCACTTATACTGTGTGACAAGACTCAATGAT 420
                                                                                                                                                                                                                                                                                                                                         ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
                                                                                                                                                                                      AACATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 466.4; DB 2;
Pred. No. 8.4e-151;
0; Mismatches 1;
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                                                                                                                                                                                                                                                     The invention relates to Parkin protein and its corresponding nucleic CC acid sequence. The nucleic acid sequence is useful for altering the proteolytic processing of Parkin at its potential cleavage site at Asp CC proteolytic processing of Parkin at its potential cleavage site at Asp CC alzheimer's disease or ischaemic stroke. It also used for detecting the CC cocurrence of proteolytic processing of Parkin at Asp 126 in a sample, in CC monitoring a potential disposition for a neurodegenerative disease, and CC for treating, preventing and/or diagnosing Parkinson's disease or other cneurodegenerative disorders. The viral vector is used for treating compounds that increase or decrease CC apoptosis. It is also used in gene therapy. The present sequence is human CC Parkin protein encoding CDNA
                                                                                                                                                                      Matches 467;
                                                                                                                                                                                  Query Match
Best Local (
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03-APR-2001;
                                                                                                                                                                                                                             Sequence 2960 BP; 815 A; 727 C; 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid sequence encoding a Parkin polypeptide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in screening assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-046812/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 68-69; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAE30800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Parkin protein; neurological disorder; apoptosis; gene therapy;
ischaemic stroke; Parkinson's disease; Alzheimer's disease; nootropic;
transgenic; cerebroprotective; neuroprotective; neurotransplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
                         121
                                                                                                                                                                                   Similarity
                                                     GGAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTTGCAAAGGCCCCTGT
                   ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
                                                                                                                GGAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCTGT
ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
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2001US-0281286P.
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102. .1499
/*tag= a
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                                                                                                                                                                                  99.0%;
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                                                                                                                                                                                  Score 466.4; DB
Pred. No. 8.4e-19
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                                                                                                                                                                                                                             720 T;
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                                                                                                                                                                      Gaps
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RESULT 5
AAD47680
ID AAD4
XX AAD4
XX AAD4
XX AAD4
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
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XX Huma
XX Huma
XX Huma
XX Huma
XX Homo
OS Synt
XX WO20
XX Homo
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The invention relates to Parkin protein and its corresponding nucleic acid sequence. The nucleic acid sequence is useful for altering the proteolytic processing of Parkin at its potential cleavage site at Asp. 126. The invention is used in manufacturing or restriction and the corresponding nucleic sequences.
                                                                                                      New isolated nucleic acid sequence encoding a Parkin polypeptide, for treating, preventing or diagnosing neurological disorders, e.c. Parkinson's disease, Alzheimer's disease or ischemic stroke, and iscreening assays.
                                                                                                                                                                                                                                      Jensen
                                                                                                                                                                                                                                                                                               29-MAR-2001;
03-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
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                                                                                                                                                                                                                                                                                                                                                                                                           WO200279459-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Parkin protein; neurological disorder; apoptosis; gene therapy; ischaemic stroke; Parkinson's disease; Alzheimer's disease; nootropic; transgenic; cerebroprotective; neuroprotective; neurotransplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-2003
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DB; AAE30801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                                                                                                                                Human
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03-JUN-2002;

2002WO-US017382

WO200299122-A1

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commodulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in CC prosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference CC activity, and detecting a test agent-blased activity of the assay system. CC also included are modulating (M2) a p53 pathway of a cell (comprising CC contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid gequence, where p53 function is restored), modulating (M3) a p53 pathway of a cell defective in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising; (a) obtaining a biological sample expression; (c) comparison indicates a likelihood disease). (M1) is useful contentifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. CC modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, anglogenesis, apoptotic or cell cromparison of the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus a anciocenic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also useful for treating defects in the p53 pathway such as angiogenic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 166-167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lc or cell proliferation disorders. The present sequence acid encoding a p53 pathway modifying protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
CACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGG
                                                                                                                                                                                           ACCTTGACCCCAGGGTCCATCTTGCTGGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
                                                                    GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCA
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                         The present sequence encodes a murine parkin2 polypeptide. The polynucleotide sequence contains a frameshift mutation, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, prion disease, Multi-system atrophy, Wilson's disease, pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of murine parkin2 with a frameshift mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 29-30;
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    Luebbert
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                                              (BIOF-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabolic
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/product= "truncated parkin2|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trauma; stroke; vascular irregularity;
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Pred. No. 7e-107;
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                                         The present sequence encodes a murine parkin2 polypeptide. The polynucleotide sequence contains a frameshift mutation, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, alzheimer's disease, Huntington's disease, pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein
Sequence 3092 BP; 818 A; 778 C; 761 G; 735 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 34-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-212797/22.
P-PSDB; AAB67530.
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Matches Query Match Best Local Local Similarity 371 675 431 735 311 615 251 191 495 435 131 384; 11 TTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGT 467 CTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGAACATCACTT CAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCTGTCAAAGAGTGC TGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGATCGGCAGTTTG GCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAACTCCCGCCACG CCCCACACTGCCCTGGGACTAGTGCAGAATTTTTTTTAAATGTGGAGCACACCCCACCT AGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTGAATGCCAAT TGATCTGTTTGGACTGTTTCCACTTGTATTGTGTCACAAGACTCAACGATCGGCAGTTTG GCATAGCGTGCACAGATGTCAGGAGCCCTGTCCTGGTCTTCCAGTGTAACCACCGTCACG CAGACAAGGACACGTCGGTAGCTTTGAACCTGATCACCAGCAACAGGCGCAGCATCCCTT CTCCAGACTGCCCTGGAACCAGAGCTGAATTTTTCTTTAAATGTGGAGCACACCCAACCT AGGGCCCATCTTGCTGGGACGATGTCTTAATTCCAAACCGGATGAGTGGTGAGTGCCAGT AGCCTGGAAAAGCTCCGAGTTCAGTGTGGCACCTGCAAACAAGCAACCCTCACCTTGGCCC CAGTTAAACCCACCTACAACAGCTTTTTCATCTACTGCAAAGGCCCCCTGCCACAAGGTCC Conservative 72.2%; 84.0%; Score 340.2; Db -, pred. No. 7e-107; Indels 0, Gaps 430 190 734 370 674 310 614 250 554 494 130 434 70

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RESULT 9
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DT 29-N
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DE Nucl
        Nucleotide sequence of murine parkin2
                           29-MAY-2001
                                                             AAF55256 standard;
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                                                             cDNA; 3253
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frameshift mutation.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a murine parkin2 polypeptide. The polypucleotide sequence contains mutations, causing Arg78 to be changed to a stop codon, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease; Huntington's disease; amyotrophic lateral scleros Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
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                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                           Similarity
CTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGAACATCACTT
                                                                                                                                                                                                   CAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCTGTCAAAGAGTGC 70
                                                                                                                                               AGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTGAATGCCAAT
                                                                                                                                                                                                                                            CAGTTAAACCCACCTACAACAGCTTTTTCATCTACTGCAAAGGCCCCTGCCACAAGGTCC
                                                  CTCCAGACTGCCCTGGAACCAGAGCTGAATTTTTCTTTAAATGTGGAGCACACCCAACCT
                                                                              CCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCACACCCCACCT
                                                                                                               AGGGCCCATCTTGCTGGGACGATGTCTTAATTCCAAACCGGATGAGTGGTGAGTGCCAGT
                                                                                                                                                                               AGCCTGGAAAGCTCCGAGTTCAGTGTGGCACCTGCAAACCAAGCAACCCTCACCTTGGCCC
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                          BP; 851 A; 818 C; 808 G; 776 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-00116766
                                                                                                                                                                                                                                                                                                                                                                                                                        associated with a less active or non-active parkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62pp;
                                                                                                                                                                                                                                                                                                                         72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.
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                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                           Score 340.2; DB 4;
Pred. No. 7.2e-107;
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parkin2"
                                                                                                                                                                                                                                                                                                                                        Length 3253;
                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                The present sequence encodes a murine parkin2 polypeptide. The polynucleotide sequence contains mutations, causing Gln38 to be changed to a stop codon, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multisystem atrophy, Wilson's disease, Pick's disease, Prion disease, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease; Huntington's disease; amyotrophic lateral scleros Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF55254 standard; cDNA;
irregularities,
protein
                                                         secondary causes inducing Parkinson's syndromes like toxins, dructumours, head trauma, stroke, vascular irregularities or metabol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 30-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkin2; Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of murine parkin2 with a frameshift mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease; 6q25.2-27; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3253
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral scleros Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                      30-AUG-1999;
                                                                                                              30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence
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                                                                    99EP-00116766
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                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                     /product= "truncated parkin2"
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Pred. No. 7.2e-107;
); Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 808 G; 776
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                                                             TGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGATCGGCAGTTTG
                                                                                                                           GCATTACGTGCACAGACGTCAGGAGCCCCCGTCCTGGTTTTCCAGTGCAACTCCCGCCACG
                                                                                                                                                                                     CTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGAACATCACTT
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      TTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGT
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Pred. No. 7.2e
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               secondary causes inducing Parkinson's syndromes like toxins, drugs, tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 36-38; 62pp; English.
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CTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAATAGTCGGAACATCACTT
                                                                                                         AGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGGTGAATGCCAAT
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                              CTCCAGACTGCCCTGGAACCAGAGCTGAATTTTTCTTTAAATGTGGAGCACACCCAACCT
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                                                                                                                                                                                                                                                                            Conservative
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/product= "truncated parkin2"
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                                                                                                                                                                                                                                                                           Score 340.2; DB 4;
Pred. No. 7.2e-107;
0; Mismatches 73;
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                                                      The present sequence encodes a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkin2on's disease in humans. The human parkin2 gene is located in gene region 625-2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral scleros; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF55244;
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a transgenic non-human animal as
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                                                                                                                                                                                                                                                                                                                                                                                                                                         62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse parkin2 protein, useful for producing las an animal model for neurodegenerative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Milson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity; ss.
                                                                                                                                                   30-AUG-1999;
                                                                                                     30-AUG-1999;
                                                                                                                                                                                                                                                    EP1081225-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGT
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                                                                                                     99EP-00116766
                                                                                                                                                   99EP-00116766
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 129. .1484
                                                                                                                                                                                                                                                                                                  /product= "truncated parkin2"
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84.0%;
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Pred. No. 7.2e-107;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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P-PSDB; AAB67533.
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                                           TGATCTGTTTGGACTGTTTCCACTTGTATTGTCACAAGACTCAACGATCGGCAGTTTG
                                                                          TGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGATCGGCAGTTTG
                                                                                                           GCATAGCGTGCACAGATGTCAGGAGCCCTGTCCTGGTCTTCCAGTGTAACCACCGTCACG
                                                                                                                                            GCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAACTCCCGCCACG
                                                                                                                                                                                                                                                                                                                                 AGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTGAATGCCAAT
                                                                                                                                                                                                                                                                                                                                                                              AGCCTGGAAAGCTCCGAGTTCAGTGTGGCACCTGCAAACAAGCAACCCTCACCTTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTTAAACCCACCTACAACAGCTTTTTCATCTACTGCAAAGGCCCCTGCCACAAGGTCC
                                                                                                                                                                             CAGACAAGGACACGTCGGTAGCTTTGAACCTGATCACCAGCAACAGGCGCAGCATCCCTT
                                                                                                                                                                                                                                             CTCCAGACTGCCCTGGAACCAGAGCTGAATTTTTCTTTAAATGTGGAGCACACCCAACCT
                                                                                                                                                                                                                                                                                                               AGGGCCCATCTTGCTGGGACGATGTCTTAATTCCAAACCGGATGAGTGGTGAGTGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 340.2; DE Pred. No. 7.2e-10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776 T; 0 U; 0 Other;
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Nucleotide sequence of a mutated

murine

parkin2

polypeptide

29-MAY-2001

(first entry)

AAF55258 standard;

cDNA; 3255

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Query Match
Best Local Similarity
Matches 384; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a murine parkin2 polypeptide. The sequence contains the mutation Lysi6lAsm. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They neurodegenerative disease such as Parkinson's disease, They neurodegenerative disease, amyotrophic lateral sclerosis, Multidisease, Huntington's disease, amyotrophic lateral sclerosis, Multisystem atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prich disease; brain tumour; head trauma; stroke; vascular irregularity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3255 BP; 852 A; 818 C; 808 G; 777 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 35-36; 62pp; English.
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DB; AAB67531.
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                              CTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGAACATCACTT
                                                                                                                                                 CCCCACACTGCCCTGGGACTAGTGCAGAATTTTTTCTTTAAATGTGGAGCACACCCCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                     CAGTTAAACCCACCTACAACAGCTTTTTCATCTACTGCAAAGGCCCCTGCCACAAGGTCC 597
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                                                                                                                   CTCCAGACTGCCCTGGAACCAGAGCTGAATTTTTCTTTAAATGTGGAGCACACCCAACCT
                                                                                                                                                                                                                                                                                                                                                       AGCCTGGAAATCTCCGAGTTCAGTGTGGCACCTGCAAACAAGCAACCCTCACCTTGGCCC
                                                                                                                                                                                                                                   AGGGCCCATCTTGCTGGGACGATGTCTTAATTCCAAACCGGATGAGIIGGTGAGTGCCAGT
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Search completed: February 25, 2005, 19:01:27 Job time : 268.776 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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US-09-949-016-983
US-09-621-976-983
US-09-601-844B-65
US-09-631-976-983
US-09-606-843-293
US-09-606-421B-293
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					Sequence 15737, A									Sequence 36816, A	Sequence 1, Appli	Sequence 1, Appli		Sequence 28, Appl

ALIGNMENTS

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APPLICANT: Shimizu, No. 6716621uyoshi
APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
FILE REFERENCE: 0652.2110000
CURRENT FILING DATE: 2000.08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 2960
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09601844B Patent No. 6716621 GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (109)...(272)
OTHER_INFORMATION: Exon
FEATURE:
NAME/KEY: misc feature
LOCATION: (836)..(972)
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NAME/KEY: misc feature
LOCATION: (514)...(635)
OTHER INFORMATION: Exo
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OTHER INFORMATION: Exon
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NAME/KEY: misc feature
LOCATION: (102)..(108)
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OTHER INFORMATION:
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LOCATION: (102)
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LOCATION: (720)..(835)
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Sequence 645, Application US/09949016
Patent NO. 6812339
GEMERRAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIC
FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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Best Local (
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LOCATION: (1387)..(2960)
OTHER INFORMATION: Exon 12
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LOCATION: (973)..(1034)
OTHER INFORMATION: Exon
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OTHER INFORMATION: Exon 10
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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR PPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 645
; LENGTH: 2960
; TYPE: DNA
; ORGANISM: Human
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                                                                                                            APPLICANT: Shimizu, No. 6716621uyoshi
APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's
FILE REFERENCE: 0652.2110000
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
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FEATURE:
NAME/KEY: CDS
LOCATION: (102)..(1
OTHER INFORMATION:
                                                               LENGTH: 2876
TYPE: DNA
ORGANISM: Homo
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               (102) .. (1412)
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Pred. No. 1.9e-154;
0; Mismatches 1;
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NAME/KEY: misc_feature LOCATION: (109)..(272) OTHER INFORMATION: NAME/KEY: misc feature

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Best Local Similarity
Matches 383; Conserv
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-09-601-844B-3
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NAME/KEY: misc feature
LOCATION: (889)...(950)
OTHER INFORMATION: EXON
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OTHER INFORMATION: Exon FEATURE:
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LOCATION: (1101)..(1184)
OTHER_INFORMATION: Exon 10
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LOCATION: (752)..(888)
OTHER_INFORMATION: Exon
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LOCATION: (1303)..(287
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                                                               CACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGG
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ilarity 81.8%;
Conservative
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US-09-949-016-982
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2007012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.2%;
Best Local Similarity 81.8%;
Matches 383; Conservative
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TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                          TCCCGCCACGTGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGAT
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Pred. No. 2.7e-91;
0; Mismatches 1;
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OF DETECTION AND
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-621-976-8976
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                         Matches
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8976, Application US/09621976 Patent No. 6639063
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 983
LENGTH: 2513
TYPE: DNA
ORGANISM: Human
                                                         Best Local
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 256;
                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
166 AACCGGATGAGTGGTGAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  502
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                                       36;
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTTCCACTTATACTGTGTGACAAGACTCAATGATCGGCAGTTTGTTCACGACCCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGGCTACTCCCTGCCTTGTGTG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGGCTACTCCCIGCCITGIGIG 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAACTCCCGCCACGTGATTTGCTTAGACT
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                                     Conservative 134; Mismatches
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                                                   8.0%; Score 37.8; DB 4
12.0%; Pred. No. 0.0069;
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Pred. No. 2.4e-78;
                                                                    DB 4;
                                   131;
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OF DETECTION AND USES THEREOF
                                                                    Length 399;
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; Sequence 65, Application US/09601844B
; Patent No. 6716621
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6716621uyoshi
APPLICANT: Mizuno, Yoshikuni
; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
; FILE REFERENCE: 0652.2110000
; CURRENT APPLICATION NUMBER: US/09/601,844B
; CURRENT PILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PCT/JP99/00545
; PRIOR FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 40
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APPLICANT: Wang, To
APPLICANT: Fan, Liq
APPLICANT: Kalos, M
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APPLICANT:
APPLICANT:
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                                                                                                                   APPLICANT:
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 RRKWMYSAGWSMMRKWTRRCASYSCWSSYCMWGAKMMYWKTSRWSYWYSSYRCTKYRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 GTTTTCCAGTGCAACTCCCGCCACGTGATTTGCTTAGACTGTTTTCCACTTATACTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AMKYWAMMKSKRSMRRRRAWYAMMYYYMARRINWGMRASCYRGAYMASAGMYYWMMYYMM 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 GCAACAAATAGTCGGAACATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 RAYWGMYTRGSKKSWRAKMSWMKKRRRRRRAWMWWKSMCWMKKSKSWWRSWGMMTKRMKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                 Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                      CCAAAGGTCCATCTTGCTGGGATGATGTTTTAATTCCA
                                                                                                                                                                                                                            Wang, Tongu
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                                                                                                                                                                                                            Kalos, Michael D.
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CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FESTESEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(361)
OTHER INFORMATION: n = A,T,C or G
US-09-643-597-293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOPTWARE: FastSEQ for Windows Version 3.0
SOPTWARE: FastSEQ for Windows Version 3.0
                                                                                RESULT 10
US-09-542-615A-293
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; Sequence 293, Application US/09480884A
; Patent No. 6482597
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Sequence 293, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 361

TYPE: DNA
ORGANISM: Homo sapien
PEATURE:
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(361)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity 59.4%;
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                                                                                                                                                                                                                                                                                                                             Match 7.4%;
Local Similarity 59.4%;
les 57; Conservative
                                                                                                                                                                                                263 CATCAGTAGCTTTGCACCTGATCGCAACAATAGTC 298
                                                                                                                                                                                                                                                                          203 CTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCACACCCCACCTCTGACAAGGAAA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 CTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCACACCCCACCTCTGACAAGGAAA 262
                                                                                                                                                                     194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 CTTGAACACGTCTTCAATTTTCCTTCCAAAATGCTGCATGCCACACTTGAGGTAACGAAG
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                                                                                                                                                                CANAAGTATTTTTAAACATGACAGCTAANAACATTC
                                                                                                                                                                                                                                                 CTTGAACACGTCTTCAATTTTCCTTCCAAAATGCTGCATGCCACACTTGAGGTAACGAAG
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APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION UNUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
INUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(361)
OTHER INFORMATION: n = A,T,C or G
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CORGANISM: Homo sapien

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(361)

OTHER INFORMATION: n = A,T,C or
US-09-542-615A-293
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                                                                                                                                                             US-09-606-421B-293
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APPLICANT: Wang, Tongton
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Micha
APPLICANT: Hangur, Chal
APPLICANT: Hosken, Manc,
APPLICANT: Fanger, Gary
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US-09-606-421B-293
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CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 361
                                                                           Query Match 7.4%;
Best Local Similarity 59.4%;
Matches 57; Conservative
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.4%;
Local Similarity 59.4%;
1es 57; Conservarion
134 CTTGAACACGTCTTCAATTTTCCTTCCAAAATGCTGCATGCCACACTTGAGGTAACGAAG 193
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                                    203 CTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCACACCCCACCTCTGACAAGGAAA 262
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Hosken, Nancy
Fanger, Gary R.
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Hosken, Nancy A.
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Kalos, Michael D.
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Pred. No. 0.076;
0; Mismatches
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                                                                           Score 34.8; DB
Pred. No. 0.076;
0; Mismatches
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298 229

263

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Milne Edwards, J.B.

LEFLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961
FILE REFERENCE: 59.USZ.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 11324
LENGTH: 405
TYPE: DM**
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CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Tongton
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Micha
APPLICANT: Bangur, Chaid
APPLICANT: Hosken, Nanc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapien
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NAME/KEY: misc_feature
LOCATION: (1)...(361)
OTHER INFORMATION: n = A,T,C or G
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Fanger, Gary R.
Li, Samuel X.
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GENERAL INFORMATION:
APPLICANT: VENTER, J. CTaig et al.
APPLICANT: VENTER, J. CTaig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/349,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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PRIOR APPLICATION NUMBER: 60/231,498
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; ORGANISM: Homo sapiens
US-09-601-844B-64
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; OTHER INFORMATION: w=a
US-09-513-999C-11324
; ORGANISM: Human
US-09-949-016-12733
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-12733/c
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US-09-601-844B-64
                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 12733
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12733, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 40
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Best Local Similarity
Matches 57; Conserv
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Best Local Similarity
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APPLICANT: Mizuno, Yoshikuni
ITILE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
FILE REFERENCE: 0652.2110000
CURRENT APPLICATION NUMBER: US/09/601,844B
CURRENT FILING DATE: 2000-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 70
                                     LENGTH: 17
TYPE: DNA
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                                                                                                     for Windows Version
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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0.038;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       466.4
466.4
466.4
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466.4
288.4
138.6
                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

23: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

25: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

26: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

27: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*

28: /cgn2_6/ptodata/1/pubpna/USOPA PUBCOMB.seq:*
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Gapop 10.0 , Gapext 1.0
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471
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       ggaagtccagcaggtagatc....actccctgccttgtgtgtag
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
  US-09-785-548-3

US-10-622-817-10

US-10-839-688-12

US-10-473-226-1

US-10-473-226-3

US-10-622-817-7

US-10-622-817-7

US-10-839-688-11

US-10-622-817-13

US-10-623-688-6
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Sequence 3, Appli
Sequence 10, Appl
Sequence 12, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 13, Appli
Sequence 6, Appli
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; LOCATION: (1)..(471)
US-09-785-548-3
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US-09-785-548-3
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Patent No. US20020155577A1
GENERAL INFORMATION:
APPLICANT: AVENTIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
FILE REFERENCE: ST00005
FILE REFERENCE: ST00005
CURRENT APPLICATION NUMBER: US/09/785,548
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 37
                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 471
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
121 ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT 180
                                         61
                                                                    61 CAAAGAGTGCAGCCGGGAAAACTCAGGGTACAGTGCAGCACCTGCAGGCAAGGCAACGCTC 120
                                                                                                                                1 GGAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAGGCCCCCTGT
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Sequence 10, Application US/10622817

Publication No. US20040214763A1

APPLICANT: CORTI, Olga
APPLICANT: HAMPE, Cornelia
APPLICANT: HAMPE, Cornelia
APPLICANT: PRADIER, Laurent
APPLICANT: PRADIER, Laurent
APPLICANT: POURNIER, Alain

ITILE OF INVENTION: METHOD FOR DETERMINING THE ABILITY OF A COMPOUND TO MODIFY THE
CURRENT APPLICATION NUMBER: US/10/622,817

FULL REFERENCE: FRAV2002-0020 US NP
CURRENT APPLICATION NUMBER: US/10/622,817

PRIOR APPLICATION NUMBER: 08 022934.5

PRIOR APPLICATION NUMBER: GB 022934.5

PRIOR APPLICATION NUMBER: US 60/396,929

PRIOR FILING DATE: 2002-12-20

PRIOR FILING DATE: 2002-07-18

SOFTWARE: Patentin version 3.2

LENGTH: 471

TYPE: DNA
ORGANISM: Homo sarians
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US-10-622-817-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(471)
                                        181 GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCA
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US-10-839-688-12
Sequence 12, Application US/10839688
Publication No. US20050014173A1
GENERAL INFORMATION:
APPLICANT: FAITES, Matthew J.
TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS
FILE REFERENCE: 07039-448001
CURRENT APPLICATION NUMBER: US/10/839,688
PRIOR APPLICATION NUMBER: US 60/468,832
PRIOR APPLICATION NUMBER: US 60/468,832
VUMBER OF SEQ ID NOS: 81
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 2955
TYPE: DNA
COGANISM: Homo sapiens
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Sequence 1, Application US/10473226

Publication No. US20040198650A1

GENERAL INFORMATION:

APPLICANT: Negene A/S

TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin

FILE REFERENCE: 506-204-00

CURRENT APPLICATION NUMBER: US/10/473,226

CURRENT FILING DATE: 2003-09-29

PRIOR APPLICATION NUMBER: DK PA 2001 00525

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 7

SOPTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 2960

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: mRNA

LOCATION: (1)..(2960)

OTHER INFORMATION:
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Sequence 3, Application US/10473226
Publication No. US20040198650A1
GENERAL INFORMATION:
APPLICANT: NeGene A/S
TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.0%;
Best Local Similarity 99.8%;
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CURRENT APPLICATION NUMBER: US/10/473,226
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: DK PA 2001 00525
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/281,286
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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US-10-622-817-7
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Best Local Similarity
 APPLICANT: CORTI, Olga
APPLICANT: HAMPE, Cornelia
APPLICANT: BRICE, Alexia
APPLICANT: BRICE, Alexia
APPLICANT: PRADIER, Laurent
APPLICANT: POURNIER, Laurent
APPLICANT: FOURNIER, Alain
APPLICANT: FOURNIER, Alain
TITLE OF INVENTION: METHOD FOR DETERMINING THE ABILITY OF A COMPOUND
TITLE OF INVENTION: INTERACTION BETWEEN PARKIN AND THE P38 PROTEIN
FILE REFERENCE: FRAV2002-0020 US NP
CURRENT APPLICATION NUMBER: US/10/622,817
CURRENT APPLICATION NUMBER: GB 0229934.5
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NAME/KEY: mRNA
LOCATION: (1)..(2960)
OTHER INFORMATION:
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TYPE: DNA
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ilarity 99.8%;
Conservative
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Pred. No. 1.1e-154;
0; Mismatches 1;
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Sequence 1, Application US/10776604

Publication No. US20050003385A1

GENERAL INFORMATION:
APPLICANT: Shimizu, Nobuyoshi
APPLICANT: Shimizu, Nobuyoshi
TITLE OF INVENTION: DANS OF Genes Participating in Parkinson's Disease
CURRENT APPLICATION NUMBER: US/10/776,604

PRIOR APPLICATION NUMBER: US/10/776,604

PRIOR APPLICATION NUMBER: 09/601,844

PRIOR APPLICATION NUMBER: 09/601,844

PRIOR APPLICATION NUMBER: PCT/JP99/00545

PRIOR FILING DATE: 1990-02-09

PRIOR APPLICATION NUMBER: UP 10/27531

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patentin version 3.1

LENGTH: 2960

TYPE: DNA
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PRIOR APPLICATION NUMBER: US 60/396,929
PRIOR FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 7
LENGTH: 2960
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: PATENTONE: PATENTONE: CDS
LOCATION: (102)..(1499)
US-10-622-817-7
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Best Local Similarity 99.8%;
Matches 467; Conservative
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Pred. No. 1.1e-154;
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NAME/KEY: misc feature

LOCATION: (1387).. (2960)

OTHER INFORMATION: Exon 12

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Best Local Similarity
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LOCATION: (1269)..(1386)
OTHER INFORMATION: Exon
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LOCATION: (1185)..(1268)
OTHER INFORMATION: Exon 10
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (514)...(635)
OTHER INFORMATION: EXON 4
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NAME/KEY: misc feature
'COATION: (836)..(972)
EXO
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OTHER INFORMATION: Exon
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LOCATION: (1035)..(118/
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OTHER INFORMATION: EXON
FEATURE:
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LOCATION: (720)...(835)
OTHER INFORMATION: Exon
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LOCATION: (636)..(719)
OTHER INFORMATION: EXON
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OTHER INFORMATION: Exon
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OTHER INFORMATION: Exon
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OTHER INFORMATION:
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LOCATION: (102)..(1496)
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240 683 180 623 120 60

563

S 밁 Ś В Ś 밁 Ś 片 Ş 망 Ś 뮍 Ś 밁 Ś

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Sequence 11, Application US/10839688
Publication No. US20050014173A1
GENERAL INFORMATION:
APPLICANT: FARTER, Matthew J.
FITTLE OF INVENTION: PARKINSON'S DISEASE MARKERS
FILE REFERENCE: 07039-448001
CURRENT APPLICATION NUMBER: US/10/839,688
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US 60/468,832
PRIOR PILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-839-688-11
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LENGTH: 2960
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                         CACCCCACCTCTGACAAGGAAACACCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGG
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                                                            TCCCGCCACGTGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGAT
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Pred. No. 1.1e-154;
0; Mismatches 1;
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; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1470)
US-10-622-817-13
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US-10-622-817-13
; Sequence 13, Application US/10622817
; Publication No. US20040214763A1
; GENERAL INFORMATION:
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SEQ ID NO 13
LENGTH: 1470
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Best Local
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APPLICANT: HAMPE, Cornelia
APPLICANT: BRICE, Alexie
APPLICANT: PRADIER, Laurent
APPLICANT: PRODER, Laurent
APPLICANT: PRODER, Laurent
APPLICANT: PROMEY, Thomas
APPLICANT: POURNIER, Alain
TITLE OF INVENTION: INTERACTION DETERMINING THE ABILITY OF A COMPOUND TO MODIFY THE
TITLE OF INVENTION: INTERACTION BETWEEN PARKIN AND THE P38 PROTEIN
FILE REFERENCE: PRAVZ002-0020 US NP
CURRENT APPLICATION NUMBER: US 10/622,817
CURRENT APPLICATION NUMBER: GB 0229934.5
PRIOR APPLICATION NUMBER: GB 0229934.5
PRIOR FILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-07-18
NUMBER: OF SEQ ID NOS: 22
NUMBER: OF SEQ ID NOS: 22
NUMBER: OF SEQ ID NOS: 22
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Local Similarity 83.9%;
nes 392; Conservative
                                                                          836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGTCCAGAAGCTAAACCCACCACCACAGCTTTTTTGTCTACTGCAAAGGCCCCTGCC 535
                      GGCAGTTTGTTCACGACCCTCAACTTGGCTACTCCCCTGCCTTGTGTG 468
                                                                                                             CCCGCCACGTGATTTGCTTAGACTGTTTCCACTTATACTGTGTGACAAGACTCAATGATC 421
                                                                                                                                                                           ACATCACTTGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTTCCAGTGCAACT 361
                                                                                                                                                                                                                                                          ACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGGA 301
                                                                                                                                                                                                                                                                                                                                           AATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTTCTTTAAATGTGGAGCAC
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                                                                            ACCGCCACGTGATCTGTTTGGACTGCTTCCACTTGTACTGTCACAAGGCTCAACGATC
                                                                                                                                                       GCATCCCCTGCATCGCGTGCACGGATGTCAGGAACCCTGTCTTGGTCTTCCAATGTAACC
                                                                                                                                                                                                                                   ACCCAACCTCAGACAAGGACACATCAGTAGCTTTGAACCTGATCACCAACAACAGCCGCA
                                                                                                                                                                                                                                                                                                                    AGTGTCAATCTCCAGACTGCCCTGGGACAAGAGCTGAATTTTTCTTTAAATGTGGAGCAC
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Pred. No. 2.7e-112;
0; Mismatches 75;
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942
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RESULT 10 US-10-776-604-3

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CURRENT APPLICATION NUMBER: US/10/776,604
CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 09/601,844
PRIOR FILING DATE: 2000-08-09
PRIOR PELING DATE: 2000-08-09
PRIOR PILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR APPLICATION NUMBER: JP 10/27531
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-03-09
PRIOR FILING DATE: 1998-03-09
PRIOR FILING DATE: 1998-03-09
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PRIOR FILING DATE: 1998-03-09
PRIOR FILING DATE: 1998-03-09
PRIOR FILING DATE: 1998-03-09
PRIOR FILING DATE: 1998-03
      Best Local Similarity
                                        Query Match
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                                                                                                                    FEATURE: misc feature NAME/KEY: misc feature LOCATION: (1303)..(2876) OTHER INFORMATION: Exon
                                                                                                                                                                                                                                              LOCATION: (1185)..(1302)
OTHER INFORMATION: Exon
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TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease
FILE REFERENCE: 0652.2110001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shimizu, Nobuyoshi
APPLICANT: Mizuno, Yoshikuni
                                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: (1185)..(130:
                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1101)..(1184)
OTHER INFORMATION: Exon 10
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OTHER INFORMATION: Exon
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LOCATION: (752)..(888)
OTHER INFORMATION: Exon
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OTHER INFORMATION: Exon 3
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OTHER INFORMATION: Exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
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OTHER INFORMATION: Exon
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LOCATION: (636)..(751)
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OTHER INFORMATION: Exon
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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                                                                                                                                                                                                                                           Exon 11
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   61.2%;
Score 288.4; DB 18; Pred. No. 2.9e-91;
                         Length 2876;
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US-10-839-688-6
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                                                                              328
                                                                                                                                                                                               268
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NUMBER OF SEQ ID NOS: 81
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 650
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: FAIREY, MATTHEW J.
TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS
FILE REFERENCE: 07039-448001
CURRENT APPLICATION NUMBER: US/10/839,688
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US 60/468,832
PRIOR FILING DATE: 2003-05-08
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10839688 Publication No. US20050014173A1
                                                                                                                                                                                              330 CAGGAGCCCCGTCCTGGTTTTCCAGTGCAACTCCCGCCACGTGATTTGCTTTAGACTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GAATGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ACCTTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGAAGTCCAGCAGGTAGATCAATCTACAACAGCTTTTATGTGTATTGCAAAAGGCCCCTGT
                         CTACTCCCTGCCTTGTGTG 468
                                                                                                              CCACTTATACTGTGTGACAAGACTCAATGATCGGCAGTTTGTTCACGACCCTCAACTTGG 449
                                                                                                                                                         CAGGAGCCCCGTCCTGGTTTTCCAGTGCAACTCCCGCCACGTGATTTGCTTAGACTGTTT
CTACTCCCTGCCTTGTGTG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCAGTTTGTTCACGACCCTCAACTTGGCTACTCCCTGCCTTGTGTG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACATCACTIGCATTACGTGCACAGACGTCAGGAGCCCCGTCCTGGTTTTCCAGTGCAAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCCCACCTCTGACAAGGAAACACCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCGCAACAAATAGTCGG
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                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                 29.4%;
                                                                                                                                                                                                                                           Score 138.6; DB 19;
Pred. No. 3.4e-38;
1; Mismatches 0;
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; LENGTH: 660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-839-688-4
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                                                                                                                                                                                                                                             ) ORGANISM: Mus musculus US-09-908-975-26043
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 26043
LENGTH: 65
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                                                                                                                                                                                  Query Match
Best Local (
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Best Local (
                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MINTZ, Liat
APPLICANT: PAIGLER, SIGONDCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: OLICONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR PILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR PILING DATE: 2000-07-28
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TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS
FILE REFERENCE: 07039-448001
CURRENT APPLICATION NUMBER: US/10/839,688
CURRENT FILING DATE: 2004-05-05
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SHOSHAN, Avi
                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 19.1%;
Local Similarity 91.3%;
les 94; Conservative
                                                                                                              227 TTAAATGTGGAGCACACCCCACCTCTGACAAGGAAACATCAGTAGCTTTGCACCTGATCG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 TTCCCAAAGGTTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 TTGACCCAGGGTCCATCTTGCTGGGATGATGTTTTAATTCCAAACCGGATGAGTGGTGAA 183
                                        287 CAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 TGCCAATCCCCACACTGCCCTGGGACTAGTGCAGWAAGTACCT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 TGCCAATCCCCACACTGCCCTGGGACTAGTGCAGAATTTTTCT 226
61 CCA 63
                                                                                                                                                             55;
                                                                                1 TTAAATGTGGAGCACACCCAACCTCAGACAAGGACACGTCGGTAGCTTTGAACCTGATCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WASSERMAN, Alon
MINTZ, Eli
MINTZ, Liat
                                                                                                                                                          Conservative
                                                                                                                                                                             10.7%;
                                                                                                                                                        Score 50.2; DB 10;
Pred. No. 3.4e-07;
0; Mismatches 8;
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Pred. No. 8.4e-21;
1; Mismatches 8;
                                                                                                                                                                                                 Length
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RESULT 14

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203 CTGGGACTAGTGCAGAATTTTTCTTTAAATGTGGAGCACCCCCACCTCTGACAAGGAAA 262

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APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455014
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-735-705-293
                                                                           US-09-735-705-293
                                                                                                                                                                                                NUMBER FAST
SOFTWARE: FAST
SEQ ID NO 293
FRIGTH: 361
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CURRENT APPLICATION NUMBER: US/10/776,604
CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 09/601,844
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCT/JP99/00545
PRIOR TILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: JP 10/27531
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
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Query Match 7.4%;
Best Local Similarity 59.4%;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 293, Application US/09735705 Patent No. US20020052329A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 65
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Mizuno, Yoshikuni
TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(361)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                   ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                       TYPE: DNA
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Hosken, Nancy
Fanger, Gary R.
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Fan, Liqun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalos, Michael D.
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 0; Mismatches
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                 Score 34.8; DB Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34.8; DB : Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                   DB 9;
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 39;
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                                                                                                                                                                                                                                                                                                                                                            THE THERAPY
                                   Length 361;
 Indels
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